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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in the Fetal liver and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_FETAL_LIVER.txt,
25 created 24 January 2001, having 25,630,231 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

Fetal liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 . The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction of
25 diseases of the liver, particularly those diseases with polygenic etiology, from diagnosis of fetal liver.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
5 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
10 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver, comprising a
15 plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,129 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
packaged separately from the genome-derived single exon
microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 12,674 - 25,129, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 12,673.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human Fetal liver which is a nucleic acid molecule
comprising a nucleotide sequence as set out in any of SEQ
ID NOs.: 1 - 12,673 or a complementary sequence or a
30 fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid expressed in the human Fetal
liver.

In one embodiment, a single exon nucleic acid
probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOs.:

12,674 - 25,129 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,130 - 37,156 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human Fetal liver, comprising:

contacting the single exon microarray in
accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human Fetal liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,129 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,674 - 25,129, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,673.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,130 - 37,156.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 25,130 - 37,156, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional
5 information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or
35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100
5 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger
10 contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was
15 erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession,
20 species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will
25 be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

30 Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the
35 National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be
35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

 Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

 In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

 Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,
25 and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

10 With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater

15 specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain

20 artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific

25 primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such

30 "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon

35 microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, 5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved 10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of 15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used 20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the 30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides 35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of
5 novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is
10 performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the
15 putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed
20 for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the
25 reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

30 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be
35 measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions
5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of
10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the
20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of
25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of
30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable
35 media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence -
5 can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process
10 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the
15 record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored
20 locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at
25 which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present
30 invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be
20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

 As earlier described, increased predictive reliability can be achieved by requiring consensus among
25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

 Although FIG. 3 shows three series of
30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as
5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including
10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right
15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of
20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing
25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using
30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during
35 amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,673 of these ORFs in Fetal liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in Fetal liver is currently available for use in measuring the level of its ORF's expression in Fetal liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, Prog. Liver Dis. 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy findings were very similar, but there were wide differences between families.

Kalra et al., Hum. Hered. 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., New Eng. J. Med. 307:271-277 (1982) described 4 white American sibs who died between ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

Cloninger, Science 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a
5 relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and
10 their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the
15 metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

20 As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with
25 development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting
30 components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL),
35 low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation).

Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary sclerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrom 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, hereditary persistence of fetal hemoglobin and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents, 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following 15 *Schistosoma mansoni* infection.

 The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have 25 genetic bases or contributions.

 Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the Fetal liver has been demonstrated are useful for both measurement in the Fetal liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. Nature 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
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"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements
5 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

10 The invention particularly provides genome-derived single-exon probes known to be expressed in Fetal liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
15 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
20 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
25 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
30 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
35 amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
15 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,674 - 25,129, respectively, for probe SEQ ID NOS. 1 - 12,673. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,674 - 25,129 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
5 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,
10 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen
15 for the common attribute of expression in the human Fetal liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell
20 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF
25 by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to
30 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-
35 derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human Fetal liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 12,673.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 12,673 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,674 - 25,129, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 12,673 can be used, or that portion thereof in SEQ ID NOS. 12,674 - 25,129 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,674 - 25,129. Such amino acid sequences are set out in SEQ ID NOS: 25,130 - 37,156. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

10 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

20 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution
5 containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC,
10 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics
15 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference
20 permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact,
25 both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when
30 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is
35 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again
5 demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray
10 experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding
20 programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual
25 display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

30 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in Fetal liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,673 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 12,673 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,673. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the
30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,674 - 25,129, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human Fetal liver and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human Fetal liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,674 to 25,129 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS... The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,673) and probe exon (SEQ ID NOs.: 12,674 - 25,129, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Fetal liver

Table 4 (526 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human Fetal liver.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Fetal liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,674 - 25,129.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single-exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,673 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Fetal liver.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,674 - 25,129 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 25,130 - 37,156, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human Fetal liver, comprising:

contacting the microarray of claim 12, with a first
collection of detectably labeled nucleic acids,
said first collection of nucleic acids derived
from mRNA of human Fetal liver; and then
10 measuring the label detectably bound to each probe of
said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:

15 algorithmically predicting at least one exon from
genomic sequence of said eukaryote; and then
detecting specific hybridization of detectably labeled
nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the Fetal liver of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:

identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
then
measuring the expression of each of said exons in a
plurality of tissues and/or cell types using
hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

- 5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,129 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,129.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,130 - 37,156.

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
475	13108	26600	4.41				
822	13535	26053	9.9				
1083	13688		2.9				
1345	13940	26462	10.32				
1656	14248	26782	2.59				
1678	14270	26803	5.03				
1763	14353	26899	1.73				
1785	14375	26919	0.89				
1792	14382	26927	9.24				
1935	14519	27075	1.21				
2021	14803	27188	3.24				
2210	14786	27360	4.38				
2318	14890	27465	2.04				
2607	15169	27735	0.89				
2607	15169	27736	0.89				
3220	15832	28311	1.65				
3498	16101	28578	1.22				
3598	16170	28652	10.28				
3617	16220		0.8				
3718	16319	28787	0.97				
4020	16818		0.84				
4275	16881	29310	1.53				
4348	16835	29378	8.4				
4368	16955	29396	0.74				
4368	16955	29397	0.74				
4430	17016		1.3				
4862	17537	29879	1.04				
5007	17580		0.59				
5054	17627	30071	0.81				
5197	17762	30187	5.95				
5212	17777	30188	1.32				
5462	18097	30415	2.1				
5462	18097	30416	2.1				
5615	18244		5.64				

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	18408		8.03				
5859	18244		4.85				
5910	18532	31267	0.84				
5915	18537	31262	3.16				
6173	24758	31552	1.41				
6200	18810	31578	1.66				
6548	19146		1.28				
6668	19264	32067	1				
6668	19264	32068	1				
7178	19711	32558	1.13				
7178	19711	32660	1.13				
7441	19965	32831	1.4				
7441	19965	32832	1.4				
8005	20547	33451	1.65				
8422	20862	33878	1.45				
8794	21333	34267	0.57				
8794	21333	34258	0.57				
9453	21878	34831	4.84				
9681	22180	35155	0.78				
9786	22284	35277	1.19				
9838	22431	35408	1.03				
10214	22709	35702	0.48				
10214	22709	35703	0.48				
10326	22820	35815	0.65				
10326	22820	35816	0.65				
10563	23088		3.06				
10725	24788	36288	2.48				
10906	23425		2.99				
11288	23769	36827	2.73				
11336	23034	36043	1.87				
11336	23034	36044	1.87				
11374	23826		2.59				
12117	24376		2.18				
12439	24578	30814	1.6				

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	18813	31593	14.37	9.8E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 16, 18, 17 and 18
7948	20490	33400	1.85	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9658	22157	35128	0.47	9.8E+00	Y18930.1	NT	Stefotobus scfaeatus 281 kb genomic DNA fragment, strain P2
9658	22157	35129	0.47	9.8E+00	Y18930.1	NT	Stefotobus scfaeatus 281 kb genomic DNA fragment, strain P2
7073	18845	32483	0.8	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7073	18845	32484	0.8	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10319	22813	35808	1.22	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 11H polypeptide 2 (Gtf2h2) genes, complete cds
10319	22813	35809	1.22	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 11H polypeptide 2 (Gtf2h2) genes, complete cds
2689	15247	27814	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2689	15247	27815	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2950	15568	28040	3.19	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8042	20584	33491	0.86	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8833	21471	34390	3.48	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP88)
5500	18134	30543	2.82	9.1E+00	AF065609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5500	18134	30544	2.82	9.1E+00	AF065609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9351	21865	30544	0.9	9.0E+00	P08241	SWISSPROT	RHODOPSIN
6186	18796	31564	5.12	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6517	19117	31907	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster OpTbx3 premature mRNA, partial cds
6517	19117	31908	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster OpTbx3 premature mRNA, partial cds
465	13099	25590	1.66	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9376	20315	33217	3.8	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (sec2a)
11048	23561		2.47	8.0E+00	P41820	SWISSPROT	BREFELIN A RESISTANCE PROTEIN
8082	20633		0.76	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7384	19910		1.95	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8302	20843	33764	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8302	20843	33765	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5968	18588	31324	3.35	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285508 5'
8688	21227	34147	2.63	7.4E+00	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8688	21227	34148	2.63	7.4E+00	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3008	15622	28089	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3008	15622	28100	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7097	18688	32507	0.7	7.2E+00	BE178080.1	EST_HUMAN	RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7203	19734	32585	1.22	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7203	19734	32586	1.22	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9516	22016		7.98	7.1E+00	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11283	23791	36848	3.2	7.1E+00	P03850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MIRDA-PHFB INTERGENIC REGION
9882	22389	35367	3.35	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11129	23637	36879	1.87	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS3
8225	20768	33884	4.06	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10253	22748	35736	1.2	6.8E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
7848	20391	33283	1.38	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5'
7849	20391	33284	1.38	6.8E+00	W03412.1	EST_HUMAN	z007c11.1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5'
9080	21597		1.13	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8
10110	22605	35595	3.85	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5488	18122		0.69	6.6E+00	Q99028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
9886	22481	35465	1.89	6.6E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9886	22481	35468	1.89	6.6E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11008	23522		2.13	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9108	21844	34594	7.21	6.5E+00	P03374	SWISSPROT	ENV POLYPEPTIDE [CONTAINS: COAT PROTEIN GP82; COAT PROTEIN GP34]
10208	22701	35695	0.49	6.5E+00	BE866001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3980969 5'
9857	22158	35127	1.11	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
10455	22949	35958	0.53	6.2E+00	6754621	NT	Mus musculus mannose 2, alpha B1 (Man2b1), mRNA
7102	19872	32511	1.34	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303 5'
9730	22228	35205	0.46	6.0E+00	AP000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (877)
10407	22901	35898	0.8	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10407	22901	35897	0.6	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
8943	19239	32042	6.87	5.8E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk18) genes, complete cds
3578	16180		1.18	5.8E+00	7881557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7215	19746	32801	0.87	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7215	19746	32802	0.87	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7570	20087		1.31	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII)
11349	23047	36059	2.68	5.0E+00	Q55278	SWISSPROT	LYCOPENE BETA CYCLASE
6399	19002	31780	0.73	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HIRCA
10858	23180		1.54	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11348	23048	36058	3.79	5.5E+00	P11980	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
11578	24024		2.08	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
7009	19507	32326	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7009	19507	32327	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7369	19895		0.72	5.4E+00	Q69435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
							VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1G;
							LIPOVITELLIN LV-2]
7811	20354		1.58	5.4E+00	Q91062	SWISSPROT	REP1 PROTEIN
8734	21273	34183	0.78	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8734	21273	34184	0.78	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9949	22444	35423	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
9949	22444	35424	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4999	17474	29830	1.52	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6814	19211		0.67	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8024	20568		3.71	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8814	21452		0.62	5.3E+00	AB034890.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp. complete cds
5655	18262		1.04	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-188-009 HT0691 Homo sapiens cDNA
10274	22769		0.78	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11074	23586		2.1	5.2E+00	Q10138	SWISSPROT	HYPOPHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
8892	21430	34354	0.88	5.1E+00	O16005	SWISSPROT	RHODOPSIN
9739	22237	35217	0.87	5.1E+00	P08182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROGICIN N IMMUNITY PROTEIN)
6430	19033	31817	0.85	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114.5
10086	22591		0.69	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509.5
10327	22821	35817	3.37	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11170	23677	36723	13.54	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10131	22828		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4135	16727		12.06	4.8E+00	AF185255.1	NT	Eucreia australis histone H3 (H3) gene, partial cds
8095	20636	33547	0.65	4.8E+00	BF367809.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8478	21017		4.95	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-504 BT0547 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
311	12966	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089718 5'
312	12966	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089718 5'
3312	15923	28398	1.08	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9124	21659	34801	1.09	4.6E+00	BE846437.1	EST_HUMAN	7e86g10.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:332088 3' similar to TR:O76140 O76140
9124	21659	34802	1.09	4.6E+00	BE846437.1	EST_HUMAN	KIAA0845 PROTEIN; contains element PTR5 repetitive element; KIAA0845 PROTEIN; contains element PTR5 repetitive element; Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10290	22785		0.77	4.6E+00	AF240796.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11474	23924	36994	1.99	4.5E+00	AE001044.1	NT	602123238F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280218 5'
11590	24039	37108	1.07	4.5E+00	BF088841.1	EST_HUMAN	602072585F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3076	15691	28164	1.53	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3076	15691	28165	1.53	4.4E+00	BF530893.1	EST_HUMAN	Murine l gene for MHC class II(a) associated invariant chain
6349	18954		1.8	4.4E+00	X13414.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
6268	18874		0.82	4.3E+00	AF059679.1	NT	Plasmodium falciparum R28R+ var 1 gene, exon 1
7464	19896	32851	2.36	4.3E+00	Y13402.1	NT	Troponeura pallidum section 38 of 87 of the complete genome
7611	20124	33001	0.84	4.3E+00	AE001222.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10741	23266	36282	8.92	4.3E+00	AF240796.1	NT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
5708	18334		3.21	4.2E+00	P16444	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5780	18405	31121	1.46	4.2E+00	P51828	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6869	19603	32435	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6869	19603	32436	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8890	21428	34353	4.95	4.2E+00	AI808013.1	EST_HUMAN	w87603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360682 3'
9832	22330	35312	2.07	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWININ PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
7168	18698	32545	0.81	4.1E+00	BE253688.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7264	19792	32848	1.7	4.1E+00	BF247839.1	EST_HUMAN	601858030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4089758 5'
7657	20169	33056	8.1	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7759	20267	33163	4.03	4.1E+00	P28994	SWISSPROT	GENE 68 PROTEIN
7759	20267	33164	4.03	4.1E+00	P28994	SWISSPROT	GENE 68 PROTEIN
7857	20308	33306	2.78	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9459	21985	34639	0.63	4.1E+00	P11253	SWISSPROT	SOS RIBOSOMAL PROTEIN L4
9590	22060	35054	2.26	4.1E+00	BF682425.1	EST_HUMAN	602247838F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333208 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10208	22703		0.5	4.1E+00	P48414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
10469	22983	36003	0.62	4.1E+00	O84242	SWISSPROT	3-OXOXOACYL-JACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
10785	23289		2.97	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLFI
10851	23372		13.84	4.1E+00	BE885880.1	EST_HUMAN	801507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:39090315
3599	16203		0.82	4.0E+00	P38228	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5650	18515	32336	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
5650	18515	32337	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7017	18515	32336	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7017	18515	32337	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7240	19769	32625	1.34	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
10070	22565	35560	0.8	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10158	22653	35647	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10158	22653	35648	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11423	23874	36937	3.99	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11423	23874	36938	3.99	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3550	16154	28636	4.78	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4413	18998		0.74	3.9E+00	AF055468.1	NT	Mus musculus seminal vesicle secretory protein 89 (MSVSP89) gene, promoter region
5839	18483	31188	3.08	3.9E+00	BE814357.1	EST_HUMAN	MFO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5839	18483	31187	3.08	3.9E+00	BE814357.1	EST_HUMAN	MFO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6746	18339	32145	0.71	3.9E+00	AF288209.1	NT	Dicystotellium discoidium non-L TR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (gag) genes, complete cds
6792	18383	32188	0.72	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6855	18532	32357	4.12	3.9E+00	P38299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7398	18823	32787	6.09	3.9E+00	M23807.1	NT	Human MHC class II lymphocyte antigen (DPw-beta-1) gene, exon 2

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.:	Exon SEQ ID NO.:	ORF SEQ ID NO.:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8259	20800	33718	2.15	3.9E+00	X65885.1	NT	X.laensis mRNA for M4 muscarinic receptor
11289	23007	36014	3.27	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11291	23743	36800	1.62	3.9E+00	AA661489.1	EST_HUMAN	nr18a12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1188318 similar to gb:A10416
2658	15217		1.1	3.8E+00	AE001562.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6525	19125	31918	0.78	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8371	20811	33631	1.06	3.8E+00	DA4725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9710	22208		0.55	3.8E+00	AJ390981.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7884
4092	16887	28144	13.56	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7218	19749		0.79	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8842	21181		0.53	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9105	21641	34581	0.68	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11308	23801	36861	3.11	3.7E+00	BF689278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36862	3.11	3.7E+00	BF689278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11767	24158	25719	1.28	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
619	13248	17482	2.6	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4917	17482		0.99	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
8487	21028	33942	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8487	21028	33943	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8579	21118	34038	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 528 of the complete genome
8578	21118	34039	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 528 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gpc), the translation start site has been verified (gpc), and repressor protein (gpr) genes, complete cds
10733	23259		4.32	3.6E+00	M86795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3284	15895	28373	1.08	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6151	18784		1.06	3.5E+00	L42898.1	NT	Yg40c08.L1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
6360	18864	31742	0.82	3.5E+00	R19745.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8421	20861		0.55	3.5E+00	P24567	SWISSPROT	zp88b04.s1 Stragene HeLa cell c3 937218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
8982	21500	34421	0.88	3.5E+00	AA190898.1	EST_HUMAN	zp88b04.s1 Stragene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
8982	21500	34422	0.88	3.5E+00	AA190898.1	EST_HUMAN	contains Alu repetitive element/contains element MSR1 repetitive element;
9414	21923	34872	1.12	3.5E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1559	14151	26883	4.49	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
2812	15174	27742	1.02	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7387	18922	32788	2.85	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7690	20188	33088	0.88	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8811	21150		0.89	3.4E+00	U85408.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
8003	21540	34470	0.7	3.4E+00	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8040	21577	34508	0.5	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10165	22860	35655	3.61	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11408	23857	36822	1.98	3.4E+00	L77670.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
6218	18828	31601	0.9	3.3E+00	Q09688	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6218	18828	31602	0.9	3.3E+00	Q09688	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7834	23876	33281	0.88	3.3E+00	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	22855	35847	0.87	3.3E+00	AP001511.1	NT	Bacillus heidelbergensis genomic DNA, section 5/14
10361	22855	35848	0.87	3.3E+00	AP001511.1	NT	Bacillus heidelbergensis genomic DNA, section 5/14
528	13158	25640	1.72	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4088	13158	25640	0.7	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4835	17413	26888	1.24	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5757	18383	31065	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5757	18383	31068	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5787	18412	31128	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5787	18412	31129	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6448	18049	31834	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6448	18049	31835	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7601	20114	32891	0.84	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7750	20258	33154	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for psb9, ycf4, ycf3, psb18 genes
7750	20258	33155	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for psb9, ycf4, ycf3, psb18 genes
8980	21498		4.84	3.2E+00	P13081	SWISSPROT	PERIPLASMIC (NIFE) HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9449	21975	34927	1.52	3.2E+00	M90383.1	NT	S. cerevisiae threonine deaminase (LDV1) gene, complete cds
10047	22542	35539	1.91	3.2E+00	AB016081.2	NT	Oryzias latipes OIG08 gene for guanylyl cyclase C, complete cds
11727	24133		4.08	3.2E+00	L33838.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
6035	18954	31398	2.24	3.1E+00	Q10135	SWISSPROT	HYPOTHEICAL 142.6 KD PROTEIN C2E2.02 IN CHROMOSOME I
7421	18945	32810	0.97	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID, PRECURSOR (C1P1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7711	20220		1.09	3.1E+00	AF303225.1	NT	<i>Bacillus subtilis</i> pectate lyase (pelE) gene, complete cds
8538	21077	33895	4.27	3.1E+00	P48894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
8538	21077	33896	4.27	3.1E+00	P48894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
9183	21760		3.77	3.1E+00	Q14857	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9249	21775	34728	0.52	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9810	22308	35282	0.75	3.1E+00	7524759	NT	<i>Chlorella vulgaris</i> chloroplast, complete genome
9899	22398		0.96	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 58.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10239	22734	35728	4.7	3.1E+00	P48385	SWISSPROT	DEOXYHYPUSINE SYNTHASE (DHS)
11338	23036		2.91	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11355	23809		7.48	3.1E+00	S58880.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PC07-MZ1, mRNA, 2871 nt]
12490	24619		1.38	3.1E+00	U77688.1	NT	<i>Brassica rapa</i> pollen coat protein homolog (BAN103) gene, complete cds
5541	18173	30588	1.68	3.0E+00	X53098.1	NT	<i>S.aureus</i> genes encoding <i>Sau981</i> DNA methyltransferase and <i>Sau981</i> restriction endonuclease
6673	18268	32073	0.72	3.0E+00	X56037.1	NT	<i>Corynebacterium glutamicum</i> frtC gene for threonine synthase (EC 4.2.99.2)
6673	18268	32074	0.72	3.0E+00	X56037.1	NT	<i>Corynebacterium glutamicum</i> frtC gene for threonine synthase (EC 4.2.99.2)
7209	18740		10.44	3.0E+00	P18408	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7247	18778		0.77	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8638	21377		1.33	3.0E+00	X87838.1	NT	<i>B.napus</i> DNA for myrosinase
10195	22890	35883	0.53	3.0E+00	Q58805	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYL TRANSFERASE) (ADOMET SYNTHETASE)
10527	23084	36075	1.62	3.0E+00	Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
10888	23409	36428	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10888	23409	36427	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
2055	14636	27207	2.32	2.9E+00	AE002225.2	NT	<i>Chlamydomonas reinhardtii</i> AR39, section 53 of 94 of the complete genome
6224	18833		0.68	2.9E+00	AB026033.1	NT	<i>Bonaparitia pediculus</i> mitochondrial DNA for 16S ribosomal RNA
6889	19487	32308	3.74	2.9E+00	Z36878.1	NT	<i>F.pristiglei</i> gdc-pA gene for P-protein of the glycine cleavage system
7262	19780	32844	4.37	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7262	19780	32645	4.37	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7479	20001	32668	6.04	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7809	20352	33280	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7809	20352	33281	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8041	20583	33490	0.89	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4153058 5'
1504	14098	26834	4.87	2.8E+00	AF186398.1	NT	Bufo marinus malarase K (malik) gene, partial cds; chloroplast gene for chloroplast product
1675	14287		3.45	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7348	18874	32740	4.88	2.8E+00	8383724	NT	Mus musculus endomucin (LOC53423), mRNA
8531	22031		0.57	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10569	19874	32740	1.68	2.8E+00	8383724	NT	Mus musculus endomucin (LOC53423), mRNA
251	12911	26394	9.31	2.7E+00	6676306	NT	Mus musculus per-hexamer repeat gene 3 (Phar3), mRNA
251	12911	26395	9.31	2.7E+00	6676306	NT	Mus musculus per-hexamer repeat gene 3 (Phar3), mRNA
5740	18368	31073	1.2	2.7E+00	LI14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8088	20628		0.8	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS8) gene including complete 5'UTR and complete cds
8868	21438		1.68	2.7E+00	AL116459.1	NT	Bethyis chirensa strain T4 cDNA library under conditions of nitrogen deprivation
8353	20282	33181	0.63	2.7E+00	AW088191.1	EST_HUMAN	xc88612x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10394	22888		1.48	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4781	17382	29812	4.97	2.6E+00	AF068749.1	NT	CMA-8T0281-031189-087-H04 BTO281 Homo sapiens cDNA
5736	18382	31068	1.94	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5736	18382	31068	1.94	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Ssx13), mRNA
5882	18812		2.42	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Ssx13), mRNA
7689	20188		5.98	2.6E+00	AF235602.1	NT	Mycobacterium fortuitum furA II gene
8003	20545	33447	1.08	2.6E+00	AJ132180.1	NT	Mus musculus SH-2-containing inositol 5-phosphatase (Ship) gene, exons 18 through 27, and complete cds
8003	20545	33448	1.08	2.6E+00	AJ132180.1	NT	fabo bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
9676	22078	35038	3.02	2.6E+00	AL161540.2	NT	fabo bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83
10257	22752		1.51	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10907	23428	36443	1.69	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12300	24988		2.78	2.6E+00	11418220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1513	14105	26840	2.29	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1513	14105	26841	2.29	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1513	14105	26841	2.29	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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5681	18601	31334	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5681	18601	31335	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6588	18601	31334	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6588	18601	31335	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6828	19418	32734	0.73	2.5E+00	D30052.1	NT	Vibrio cholerae cbaA gene and cbaB gene for cholera toxins, complete cds
7736	20244	33135	1.05	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
9032	21568	34498	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9766	27264	35247	0.88	2.5E+00	BE287798.1	EST_HUMAN	601175779F1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:3531030 5'
11724	24131		1.88	2.5E+00	AF289885.1	NT	Mus musculus EIF-4H1 gene, partial cds; LMK1 gene, complete cds; and ELN gene, partial cds
3047	15663	28144	0.9	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' and
5033	17607	30052	6.78	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6161	18774	31536	4.02	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
8082	20624	33536	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8082	20624	33537	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8153	20694		2.33	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8585	21124		1.62	2.4E+00	AW875128.1	EST_HUMAN	RC2.PT0004-031299-011-405 PT0004 Homo sapiens cDNA
8762	21301	34222	8.16	2.4E+00	P24081	SWISSPROT	ENDOCHITININASE B PRECURSOR (CHIN-B)
8951	22446	35427	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
8951	22446	35428	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10017	22512	35504	1.62	2.4E+00	X02511.1	NT	H.sapiens CTGF gene and promoter region
10141	22636		7.38	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
10225	22720	35710	1.63	2.4E+00	BE326702.1	EST_HUMAN	hr63108.x1 NCI_OGAP_KiH11 Homo sapiens cDNA clone IMAGE:3133187 3'
10225	22720	35711	1.63	2.4E+00	BE326702.1	EST_HUMAN	hr63108.x1 NCI_OGAP_KiH11 Homo sapiens cDNA clone IMAGE:3133187 3'
10483	22977	35988	1.27	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
10958	23473	36498	1.69	2.4E+00	Y14070.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: gtpPKD operon and downstream
11237	23768	36826	2.27	2.4E+00	AF159853.2	NT	Fragaria x anemassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1298	13890	26413	11.15	2.3E+00	Z46724.1	NT	G domesticus artificial single chain antibody gene (L3)
4189	16786		1.65	2.3E+00	AJ401081.1	NT	Bos taurus parval cyto gene for cytochrome b
6000	18620		0.91	2.3E+00	N88245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7477	18999	32864	2.54	2.3E+00	6878554	NT	PROLYLCARBOXYPEPTIDASE
7593	25120		4.61	2.3E+00	P07169	SWISSPROT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7756	20284	33159	1.09	2.3E+00	X60285.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
							M.musci dnak and chak genes homologues coding for Dnak and Dnal

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9038	21575	34505	0.53	2.3E+00	5835317	NT	Polyporus ornatiopsis mitochondrion, complete genome
9097	21833	34572	1.79	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10681	21213	34224	2	2.3E+00	Q07076	SWISSPROT	(FUCOSYLTRANSFERASE 4) (FUCT-IV)
11612	24055	37119	2.82	2.3E+00	BF541987.1	EST_HUMAN	ANNEXIN VII (SYNEXIN)
11612	24055	37120	2.82	2.3E+00	BF541987.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11850	24278	31020	7.31	2.3E+00	BE885237.1	EST_HUMAN	602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
4089	16885	29143	91.07	2.2E+00	AF020528.1	NT	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5'
4403	16888	29432	4.5	2.2E+00	D87071.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4403	16888	29433	4.5	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							Rat gene for regucalcin, exon1 (non-coding exon)
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5545	18177	30581	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5545	18177	30582	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
6016	18635	31373	0.95	2.2E+00	BE827220.1	EST_HUMAN	RC3-CT0254-300800-022-406 CT0254 Homo sapiens cDNA
6016	18635	31374	0.85	2.2E+00	BE827220.1	EST_HUMAN	RC3-CT0254-300800-022-406 CT0254 Homo sapiens cDNA
6212	18822	31583	9.1	2.2E+00	BE250383.1	EST_HUMAN	600843401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6495	18098	31880	4.32	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MJ-2
6709	19503	32107	3.04	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7037	18057	32147	3.58	2.2E+00	AA894574.1	EST_HUMAN	n895602.a1 NC1_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1058378 3'
7358	18884	32747	0.9	2.2E+00	AA137027.1	EST_HUMAN	2787704.f1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:586143 5'
7602	20115	32882	25.23	2.2E+00	AA46012.1	EST_HUMAN	z05g10.f1 Soares_tad_fetus_Nb21F8_9w Homo sapiens cDNA clone IMAGE:785634 5'
8046	20588	33494	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45838 Mouse mRNA for nuclear pore-targeting component of (MOUSE);
8046	20588	33495	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45838 Mouse mRNA for nuclear pore-targeting component of (MOUSE);
9265	21791		12.17	2.2E+00	BE741678.1	EST_HUMAN	mRNA for nuclear pore-targeting complex component of (MOUSE);
9488	24783		2.57	2.2E+00	Q04708	SWISSPROT	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9868	22481	35443	1.98	2.2E+00	AI280373.1	EST_HUMAN	TRANSPONSON TY1 PROTEIN A
							qnt68603.x1 Soares_placenta_8to9weeks_2NdtIP8to9w Homo sapiens cDNA clone IMAGE:1883965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9898	22461	35444	1.96	2.2E+00	A120073.1	EST_HUMAN	qm88003.x1 Soares_plecanta_860weeks_2NhrHP81c9W Homo sapiens cDNA clone IMAGE:1883985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10008	22503	35494	3.7	2.2E+00	BF248782.1	EST_HUMAN	801855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10353	22847	35941	2.99	2.2E+00	AF163416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein HGR74 homolog mRNA, complete cds
11316	23014	36023	4.01	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11482	23832	37003	4.23	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
585	15419	25689	0.28	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3648	18251		0.65	2.1E+00	AW446366.1	EST_HUMAN	UHH-B13-ak-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6281	18889		0.85	2.1E+00	P76357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6889	19633	32471	3.38	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7110	19450	32268	5.13	2.1E+00	N26575.1	EST_HUMAN	Y08a10.s1 Soares_melanocyte_2NhrHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8434	20974		2.27	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
10454	22948		0.58	2.1E+00	Y10284.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1238	13838	26352	1.3	2.0E+00	AF180527.1	NT	H. sapiens TRAF1 gene, putative promoter region
1238	13836	26353	1.3	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1380	13973	26501	0.92	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1619	14212		2.89	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Net-K+-ATPase beta 1 subunit mRNA, complete cds
2184	14770	27343	3.89	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2184	14770	27344	3.89	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4176	16787	28215	1.9	2.0E+00	AW684496.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I
4176	16787	28216	1.9	2.0E+00	AW684496.1	EST_HUMAN	H13005.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677
7552	20071		0.77	2.0E+00	P07568	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7867	20509	33415	3.56	2.0E+00	AB0008876.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7867	20509	33416	3.56	2.0E+00	AB0008876.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7867	20509	33417	3.56	2.0E+00	AB0008876.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8853	21392	34314	3.62	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12295	24946	30622	7.77	2.0E+00		NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5784	18409	31124	6.88	1.9E+00	5834843	NT	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
5784	18409	31125	6.88	1.9E+00	6754388	NT	Gallus gallus mitochondrion, complete genome
6249	18858	31630	1.2	1.9E+00	BE968695.1	EST_HUMAN	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itp1r1), mRNA
							Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itp1r1), mRNA
							601679036F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6760	19353		1.02	1.8E+00	AW845689.1	EST_HUMAN	MR0-CT0063-071069-002-q02 CT0063 Homo sapiens cDNA
6845	19435		2.31	1.8E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8396	20638	33859	2.16	1.8E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8396	20638	33859	2.16	1.8E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8593	21132		2.45	1.8E+00	BF360208.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
8825	21384		1.35	1.8E+00	Q51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
							ab94e04.s1 Streptococcus sp. (837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element ;
9648	22048	35009	0.6	1.8E+00	AA689125.1	EST_HUMAN	Homo sapiens gag-pro-pod precursor protein gene, partial cds
10459	22950	35959	0.52	1.8E+00	AF248269.1	NT	PROTEIN B8 PRECURSOR
3128	15742	28211	1.88	1.8E+00	P21004	SWISSPROT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3154	15788	28234	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3154	15788	28235	2.42	1.8E+00	U04356.1	NT	(atpE) genes, complete cds
6027	18646		2.02	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6253	18862	31634	2.02	1.8E+00	BF311869.1	EST_HUMAN	601887854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127394 5'
6532	19132		1.53	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298272 5'
6838	19428	32244	1.35	1.8E+00	BF305652.1	EST_HUMAN	601883488F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7119	19459	32274	1.08	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8060	20602	33512	0.81	1.8E+00	P11369	SWISSPROT	ENDONUCLEASE]
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8060	20602	33513	0.81	1.8E+00	P11369	SWISSPROT	ENDONUCLEASE]
8788	21327	34252	2.12	1.8E+00	Q43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9102	21638	34577	0.63	1.8E+00	R31042.1	EST_HUMAN	YH72a08.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9186	21703	34845	0.8	1.8E+00	AW880004.1	EST_HUMAN	QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
9763	22261	35244	0.87	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10163	22678		3.78	1.8E+00	AF111849.1	NT	Homo sapiens PRO5530 mRNA, complete cds
10447	22941		0.85	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
							Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12076	24915		6.85	1.8E+00	AF314254.1	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
12163	24403		4.96	1.8E+00	9508404	NT	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
12476	24815	30790	1.38	1.8E+00	BF212412.1	EST_HUMAN	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	13750	20259	2.08	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
2311	14883	27458	2.37	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2411	14878	27554	1.29	1.7E+00	AI141087.1	EST_HUMAN	aa43h05.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1878137 3'
4558	17141	29580	0.74	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
5787	18422	31137	1.65	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171289-127-c05 BT0282 Homo sapiens cDNA
5787	18422	31138	1.65	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171289-127-c05 BT0282 Homo sapiens cDNA
6168	18780	31545	3.35	1.7E+00	Q81TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7270	19768	32654	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7270	19768	32655	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7308	19834	32693	1.63	1.7E+00	P20393	SWISSPROT	ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA)
7786	20339	33247	0.96	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 2 and gamma 4 gene clusters
7876	20518	33425	1.34	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tall), mRNA
8008	20548	33452	0.57	1.7E+00	BF530830.1	EST_HUMAN	602071917F-1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4214689 5'
8478	21018	33933	0.61	1.7E+00	AF245613.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8502	21101	34088	2.08	1.7E+00	BF308000.1	EST_HUMAN	601894256F-1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8638	21177	34088	0.49	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8638	21177	34087	0.49	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9076	24792	34545	2.25	1.7E+00	Q60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9076	24792	34546	2.25	1.7E+00	Q60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
9524	22024	36885	1.65	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
11467	23917	36885	2.16	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp508I-cleaved sublibrary Homo sapiens cDNA not directional
12030	24320	30993	1.52	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
12558	24659	30873	1.79	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element ;
2078	14858	27229	21.82	1.6E+00	AF198339.1	NT	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1
2087	14888	27238	4.3	1.6E+00	AF077374.1	NT	repetitive element ;
2083	14673	27243	1.04	1.6E+00	Y11944.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2323	14894		1.13	1.6E+00	X98373.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2888	15804	28094	1.5	1.6E+00	W58426.1	EST_HUMAN	Mus musculus ST6GalNAcII gene, exon 2
- 4104	16898		7.23	1.6E+00	BF570077.1	EST_HUMAN	Mus musculus gene encoding endo-polygalacturonase
							B. napus gene encoding endo-polygalacturonase
							ztd25f01.r1 Soares_fetal_heart_NhhH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
							gb:D29805 N-ACETYL-LACTOSAMINE SYNTHASE (HUMAN);
							602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4444	17030	28470	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4444	17030	28471	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5145	17715	30145	0.6	1.6E+00	AF075394.1	NT	Urbauthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5145	17715	30146	0.6	1.6E+00	AF075394.1	NT	Urbauthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5243	17807	30229	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5993	18813	31347	1.95	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2701 gene, 3' end
6072	18889	31434	0.82	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
6596	19180	31988	0.83	1.6E+00	BF380703.1	EST_HUMAN	IL2-JT0073-060800-146-E02 UT0073 Homo sapiens cDNA
6811	19402	32218	1.07	1.6E+00	AW294881.1	EST_HUMAN	UHL-BI2-af-b-04-0-JL.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7293	19821	32680	2.32	1.6E+00	BE5897287.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
7873	20315		1.09	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8320	20881	33786	3.24	1.6E+00	AJ287131.1	NT	Mus musculus SIL, MAP 17, CYP a, SCL & CYP b genes
8831	21370	34294	0.85	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8831	21370	34295	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9381	24790	33221	3.18	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9381	24790	33222	3.18	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
9649	22148	35119	1.34	1.6E+00	T41280.1	EST_HUMAN	ph658_18NTV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph658_18NTV
10052	22547	35541	0.52	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a1 (IAL), and zinc finger protein (DNZ1) genes, complete cds
10088	22583	35575	0.92	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0018-080200-100-d07 LT0018 Homo sapiens cDNA
10088	22583	35576	0.92	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0018-080200-100-d07 LT0018 Homo sapiens cDNA
10246	22741	35731	0.49	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10650	23182	36196	1.59	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) : CAPSID ASSEMBLY PROTEIN]
10688	23216	36228	1.56	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) : CAPSID ASSEMBLY PROTEIN]
10723	18889	31434	6.41	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
11552	24000	37072	2.82	1.6E+00	AF104913.1	NT	Homo sapiens unknown mRNA
35	12714	25173	4.02	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
252	12912	25396	2.17	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome
649	13272		1.88	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardisin) (Adam15), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1960	14544	27101	2.55	1.5E+00	AF275265.1	NT	Mus musculus receptor protein tyrosine phosphatase-rho (Ptp-rho) gene, exons 10 and 11 and partial cds
2454	15021	27592	2.13	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2558	15120	27690	1.83	1.5E+00	6878360	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3172	15021	27592	1.54	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3421	16029	28510	0.7	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 228 of the complete chromosome 1
5803	18525	31250	0.94	1.5E+00	A1855301.1	EST_HUMAN	h12110.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.;
5803	18525	31251	0.94	1.5E+00	A1855301.1	EST_HUMAN	h12110.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.;
6538	18137	31830	2.68	1.5E+00	R17879.1	EST_HUMAN	y010602.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31683 5'
7182	19714		1.37	1.5E+00	BE785358.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7214	19745	32599	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7214	19745	32600	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7383	18609	32774	1.02	1.5E+00	AA989259.1	EST_HUMAN	ak28110.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
8065	20807	33519	0.85	1.5E+00	BE987448.1	EST_HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8578	21117	34037	1.1	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
8948	21484		0.53	1.5E+00	AB038518.1	NT	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9061	21598	34528	0.54	1.5E+00	BF217818.1	EST_HUMAN	601882662F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4085135 5'
9404	21813	34862	0.9	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2h4P Homo sapiens cDNA clone IMAGE:147697 5'
9553	22053	35018	1.12	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-281099-008-d09 GT0192 Homo sapiens cDNA
9774	22272	35257	5.97	1.5E+00	BF378754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
9885	22480		1.47	1.5E+00	BF337044.1	EST_HUMAN	602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'
10098	22583	35585	2.85	1.5E+00	AA017889.1	EST_HUMAN	z638g08.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381308 5'
10098	22583	35588	2.85	1.5E+00	AA017889.1	EST_HUMAN	z638g08.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381308 5'
11277	23790	36785	4.1	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547P243 3'
11418	23887		8.57	1.5E+00	X07390.1	NT	Malze mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
12022	25010	30015	1.59	1.5E+00	D63480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12255	24465		4.99	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
32	12711	25169	1.8	1.4E+00	7681685	NT	Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA
32	12711	25170	1.8	1.4E+00	7681685	NT	Homo sapiens DKFZP588M0122 protein (DKFZP588M0122), mRNA
1774	14384	26809	1.32	1.4E+00	H19859.1	EST_HUMAN	yn57e03.r1 Soares adult brain N2b5-4B55Y Homo sapiens cDNA clone IMAGE:172540 5'
2316	14888		0.98	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (gluA) gene, complete cds
2372	14942		7.8	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2693	15250	27820	1.45	1.4E+00	X74483.1	NT	Human papillomavirus type 7 genomic DNA
2802	15354	27822	2.79	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2802	15354	27823	2.79	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3376	15685		0.68	1.4E+00	5453733	NT	Human sapiens Mad4 homolog (MAD4) mRNA
4342	16929	28369	1.14	1.4E+00	AW900455.1	EST_HUMAN	CMV-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA
4342	16929	28370	1.14	1.4E+00	AW900455.1	EST_HUMAN	CMV-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA
4685	17267		1.78	1.4E+00	BF681547.1	EST_HUMAN	602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287558 5'
5575	18208	30657	1.78	1.4E+00	AW054978.1	EST_HUMAN	wt45g07.x1 NCJ_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5719	18345		5.04	1.4E+00	AB032883.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6425	19028	31811	2.73	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6437	25116		4.4	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0805 protein, complete cds
6544	19143	31936	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6544	19143	31937	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6683	19181	31981	0.67	1.4E+00	11066333	NT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6811	19570	32398	0.77	1.4E+00	AW883057.1	EST_HUMAN	CM3-NN0008-300300-132-b12 NN0008 Homo sapiens cDNA
7330	19857	32720	2.31	1.4E+00	AJ133269.1	NT	Homo sapiens catenin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7343	19870	32735	1.1	1.4E+00	AW407700.1	EST_HUMAN	haz3f05.x1 NCJ_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2816873 3' similar to contains Alu repetitive element;
8277	20818		0.68	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8728	21208		4.01	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9023	21560	34487	2.13	1.4E+00	R20459.1	EST_HUMAN	y933f12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9125	21680	34603	3.72	1.4E+00	BE084887.1	EST_HUMAN	RC1-BT0313-301289-012-f05 BT0313 Homo sapiens cDNA
9158	21683	34637	0.58	1.4E+00	AF134944.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10109	22804	35594	0.77	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10160	22845	35637	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0188-281089-008-C04 HT0188 Homo sapiens cDNA
10150	22845	35638	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0188-281089-008-C04 HT0188 Homo sapiens cDNA
10418	22912	35912	1.11	1.4E+00	D63441.1	NT	Pandora colananae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10418	22912	35913	1.11	1.4E+00	D63441.1	NT	Pandora colananae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10848	23463	36485	2.16	1.4E+00	AA195528.1	EST_HUMAN	zr36e09.r1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:685512 5' similar to contains element MER22 repetitive element;

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11104	23614	36854	6.28	1.4E+00	AB006882.1	NT	Homo sapiens APECEB mRNA for AIRE-1, complete cds
11283	23736	36781	3.92	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11283	23736	36782	3.92	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11304	23797	36855	3.19	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11304	23797	36856	3.19	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11865	24935		2.43	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12287	25108		2.38	1.4E+00	11645838	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen sa70-2 (SE70-2), mRNA
598	13225		1.38	1.3E+00	Z79640.1	NT	M.mucedo gene encoding 4-Dihydroxymethyl-trisporate dehydrogenase
935	13548	26065	2.33	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1168	13770		22.19	1.3E+00	Y19213.1	NT	Homo sapiens putative psalHbA pseudogene for hair keratin, exons 2 to 7
1340	13935	26456	13.67	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1340	13935	26457	13.67	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1400	13994		1.05	1.3E+00	U81730.2	NT	Cox lacryme-habi dihydrodipicolinate synthase (dispa) gene, complete cds
1653	14245		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2285	14859		1.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPs and MASPs genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2586	15149		0.97	1.3E+00	BE968735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3815945 3'
2868	15581	28080	0.98	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
3657	16260	28732	0.91	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
4713	15581	28080	1.31	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5705	18331	30835	1.08	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
6169	18781	31546	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0288-291189-004-f08 CT0289 Homo sapiens cDNA
6169	18781	31547	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0288-291189-004-f08 CT0289 Homo sapiens cDNA
6549	19147	31943	1.24	1.3E+00	M33498.1	NT	O.melanogaster no-on-transient A gene product, complete cds
6847	19437		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6926	19595	32415	0.85	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7033	19587	32394	1.01	1.3E+00	BE538819.1	EST_HUMAN	601081420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7157	19889	32533	0.79	1.3E+00	BE243571.1	EST_HUMAN	TCBAP-ID0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TCBAP0959
7481	20003	32868	3.97	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8239	20780	33701	2.08	1.3E+00	AJ008912.1	NT	Sus scrofa pib gene
8384	20824	33844	2.54	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
8486	21035	33856	0.89	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8844	21183		1.57	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8725	21284	34184	0.88	1.3E+00	AI927829.1	EST_HUMAN	wc85a07.x1 NCI CGAP_KJ411 Homo sapiens cDNA clone IMAGE:2462100 3'
8073	21610	34540	0.48	1.3E+00	H42881.1	EST_HUMAN	y088c03.s1 Soares breast 3NtHb1st Homo sapiens cDNA clone IMAGE:183078 3'
9073	21610	34541	0.48	1.3E+00	H42881.1	EST_HUMAN	y088c03.s1 Soares breast 3NtHb1st Homo sapiens cDNA clone IMAGE:183078 3'
9434	21980		4.54	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9443	21989	34917	2.12	1.3E+00	X72019.1	NT	S. alba phr-1 mRNA for photolyase
9443	21989	34918	2.12	1.3E+00	X72019.1	NT	S. alba phr-1 mRNA for photolyase
9542	22042	35003	1.1	1.3E+00	AF050250.1	NT	Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds
9588	22088	35052	1.62	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9685	22184	35137	1.21	1.3E+00	AI927829.1	EST_HUMAN	wc85a07.x1 NCI CGAP_KJ411 Homo sapiens cDNA clone IMAGE:2462100 3'
9740	22238	35218	0.83	1.3E+00	AJ223982.1	NT	Lactococcus lactis cremoris NCDO-11v1 chromosomal inversion junction DNA
9740	22238	35219	0.83	1.3E+00	AJ223982.1	NT	Lactococcus lactis cremoris NCDO-11v1 chromosomal inversion junction DNA
9780	22278	35263	3.85	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
10114	22609	35600	1.25	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10130	22625	35615	2.41	1.3E+00	M28953.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10476	22970		0.85	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10504	22988		0.52	1.3E+00	8923637	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
10507	23001	36008	0.48	1.3E+00	H42881.1	EST_HUMAN	y088c03.s1 Soares breast 3NtHb1st Homo sapiens cDNA clone IMAGE:183078 3'
10507	23001	36009	0.48	1.3E+00	H42881.1	EST_HUMAN	y088c03.s1 Soares breast 3NtHb1st Homo sapiens cDNA clone IMAGE:183078 3'
10573	23108		4.68	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
10785	23309	36316	2.3	1.3E+00	P25298	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10807	23330	36342	2.17	1.3E+00	Z16892.2	NT	Mus musculus desatin gene
11216	23718		1.87	1.3E+00	AW274791.1	EST_HUMAN	XP00603.x1 NCI CGAP_HJN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11414	23865	36926	3.09	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11488	23937	37007	3.09	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.6kb fragment
12011	24312		3.63	1.3E+00	AF187873.1	NT	Caixa porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds

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12182	24423	30849	3.47	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCJ CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452 5'
12204	24828		1.78	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12303	24500		2.08	1.3E+00	AF187035.1	NT	Stamira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
12673	24904		1.25	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
678	13302	25784	9.75	1.2E+00	AA678246.1	EST_HUMAN	2122008.at Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
858	13472	25883	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13472	25884	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13472	25885	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
911	13524		1.9	1.2E+00	8824234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077). mRNA
1203	13803	26316	4.87	1.2E+00	AF080245.2	NT	Eleis claffera sesquiterpene synthase mRNA, complete cds
1247	13844	26361	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1247	13844	26362	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2054	14635	27308	53.59	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
2417	14985	27559	1.53	1.2E+00	AF156486.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3144	16758	28224	1.16	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3201	15813	28287	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3201	15813	28288	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3325	15935		3.43	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3399	16007	28488	0.57	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3774	16374	28639	8.66	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4058	16855	29121	1.87	1.2E+00	BF373570.1	EST_HUMAN	MRO-F10175-050800-203-g08_1 FT0175 Homo sapiens cDNA
4388	16907	28489	1.12	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4570	17153		2.09	1.2E+00	M87000.1	NT	Rattus norvegicus cardiac AE3 gene, exons 1-23
4621	17204	28653	1.08	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4659	17241	28695	1.5	1.2E+00	AF158405.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4680	17272		9.41	1.2E+00	Y08200.1	NT	T. pinnastrum chloroplast rbcL gene, partial
4791	18008		0.77	1.2E+00	M81778.1	NT	G. gallus T-cadherin mRNA, complete cds
5628	18258	30728	1.08	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5743	18389	31077	2.27	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6034	18653	31395	0.72	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6300	18808	31679	2.17	1.2E+00	X74885.1	NT	D. hydei ey1 repeat cluster DNA, fragment D
6361	18865	31743	3.98	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-e03 BN0090 Homo sapiens cDNA
6433	19036	31822	1.43	1.2E+00	X88084.1	NT	C. glutamicum pls gene and ackA gene
6433	19036	31823	1.43	1.2E+00	X88084.1	NT	C. glutamicum pls gene and ackA gene

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6475	18078	31859	34.98	1.2E+00	AA756254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
6628	18225	32030	2.26	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6895	19493	32314	1.18	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7007	19505	32324	2.8	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7300	19828		0.8	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7417	24782	32808	1.59	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7846	20158	33045	2.84	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
8504	21043	33984	3.05	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
8597	21138	34051	0.69	1.2E+00	P38427	SWISSPROT	Homo sapiens CGI-30 protein (LOC51611), mRNA
8809	21348		0.53	1.2E+00	7708271	NT	MR2-CT0222-201089-001-e07 CT0222 Homo sapiens cDNA
8955	21483	34416	2.03	1.2E+00	AW377210.1	EST_HUMAN	IR communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9319	21833	34783	2.92	1.2E+00	Z32850.1	NT	
9523	22023	34981	1.96	1.2E+00	D11745.1	EST_HUMAN	HUMHMD1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
9844	22342	35324	3.47	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific endase
10229	22724		0.67	1.2E+00	AB008668.1	NT	Homo sapiens kiofno gene, exon 1
11224	23755	36813	2.19	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0284-161189-001-d01 ST0284 Homo sapiens cDNA
11262	23780		6.64	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11331	23029	36038	3.76	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
11976	24907	30712	32.4	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11988	24304		2.11	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 8/14
489	13122	25608	1.19	1.1E+00	D66980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1786	14389	26934	1.48	1.1E+00	AW695383.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
2617	15179	27748	1.09	1.1E+00	AF087124.1	NT	Wheat yellow mosaic virus RNA1 270 kDa precursor protein gene, complete cds
3373	15681	28458	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15681	28459	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3533	16138	28620	0.84	1.1E+00		NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
					8922641	NT	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12898 P53-BINDING PROTEIN 53BP1 ;
3639	16242	28718	1.06	1.1E+00	AB083680.1	EST_HUMAN	Xyella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28845	1.41	1.1E+00	AE003986.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28846	1.41	1.1E+00	AE003986.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3889	16488		0.61	1.1E+00	X85374.1	NT	H.parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4016	16814	29087	0.67	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4093	16888	28145	0.95	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4295	16881		7.81	1.1E+00	5835331	NT	R. uniconis complete mitochondrial genome
5131	17703	30137	3.54	1.1E+00	U18488.1	NT	African swine fever virus, complete genome
5132	17704	30138	0.96	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5201	17768	30180	1	1.1E+00	U34740.1	NT	Emeticella nidulans starigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcI), (stcJ), (stcK), (stcL), (stcO), (stcQ), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5230	17794	30213	0.96	1.1E+00	X78425.1	NT	E. faecalis pbp5 gene
5409	17866		1.04	1.1E+00	AE003868.1	NT	Xylella fastidiosa, section 15 of 229 of the complete genome
5510	18143	30555	1.52	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5798	18423	31139	18.98	1.1E+00	BE980184.1	EST_HUMAN	601652778R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5815	18439	31161	3.23	1.1E+00	AI138582.1	EST_HUMAN	q85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738260 3'
6242	18851	31821	1.25	1.1E+00	11418739	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter), member 14 (SLC8A14), mRNA
6420	19023	31807	0.71	1.1E+00	AF197881.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6539	19138	31931	0.71	1.1E+00	R06037.1	EST_HUMAN	ye89e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124824 5'
6817	19408	32225	0.7	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 68 (EP68 gene)
7338	19885	32729	0.78	1.1E+00	X55081.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7501	20023	32898	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7501	20023	32887	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7521	20041	32810	9.72	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7580	24787	32973	0.99	1.1E+00	11967860	NT	Mus musculus silent mating type information regulation 2 (S.cerevisiae, homolog)-like (Sir2), mRNA
8074	20616	33530	2.8	1.1E+00	BF683896.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5'
8163	20704	33620	0.76	1.1E+00	AI478339.1	EST_HUMAN	tm39h1.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2180549 3'
8672	21211	34150	0.75	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COX-like gene
8749	21288	34208	0.78	1.1E+00	S90750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region (human, mRNA Partial, 375 nt)
8958	20297		0.88	1.1E+00	BE384678.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9546	22048	35007	0.88	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9599	22099		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9887	22186	35160	0.84	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9747	22245	35228	1.59	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
9850	22348	35330	4.82	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9809	22408	35381	19.39	1.1E+00	8754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10395	22889	35883	1	1.1E+00	P73789	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10530	23067	36079	2.93	1.1E+00	11067364	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
10586	23121		4.06	1.1E+00	AF068942.1	NT	Klebsiella fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
10978	18026		5.28	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
10983	23497	36526	3.78	1.1E+00	AF012882.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
10983	23497	36527	3.78	1.1E+00	AF012882.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11234	23765	36822	6.02	1.1E+00	AI809698.1	EST_HUMAN	w78611.x1 Source_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11946	24275		1.82	1.1E+00	P07890	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12051	24335	30897	2.25	1.1E+00	AF216898.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12184	24803		1.64	1.1E+00	AF234169.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
103	12779		3.22	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
118	12789	25271	3.48	1.0E+00	D88425.1	NT	Canis caryacus mRNA for serine/threonine kinase, complete cds
443	13078		2.14	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
602	13231	25704	1.53	1.0E+00	AJ251660.1	NT	Girardinus tigrina mRNA for homeodomain transcription factor (so gene)
705	13326	25813	7.12	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
707	13328		0.89	1.0E+00	AF125884.1	NT	Aedes aegypti much-like protein MUC1 mRNA, complete cds
1429	15441		1.73	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1794	14394	26929	0.91	1.0E+00	AB006531.1	NT	Plautia stali interline virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2528	15080	27682	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2528	15080	27683	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2800	15517	27886	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2800	15517	27987	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2884	15610		0.83	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN CBF12.08C IN CHROMOSOME 1
3232	15844	28324	0.91	1.0E+00	AA628453.1	EST_HUMAN	af28608.s1 Source_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032630 3' similar to WP:CA2D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;

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3659	12779		0.78	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3744	16345	28813	1.55	1.0E+00	AJ223818.1	NT	Agaricus bisporus mRNA for tyrosinase
4144	16736	28189	1.5	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4362	16849		0.84	1.0E+00	8822245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5165	17734		17.2	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5339	17800		0.6	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5432	18010	30394	1	1.0E+00	AB038022.1	NT	Oncorhynchus mykiss sII1 mRNA for rhamnose binding lectin STL1, complete cds
5486	18120	30527	2.56	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6013	18633	31368	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6013	18633	31369	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6111	18727	31480	1.22	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6263	18871	31841	4.41	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6269	18877	31845	1.56	1.0E+00	AW452782.1	EST_HUMAN	UHL-B13-alk-4-09-Q-U1.s1 NCI_CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6615	19212	32018	1.79	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6662	19258	32062	0.83	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6742	19336		1.5	1.0E+00	P46508	SWISSPROT	SRB-11 PROTEIN
6874	19608	32442	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxpsin
7182	19724	32573	1.22	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7493	20016		8.58	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7697	20208	33093	1.36	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7710	20219	33107	7.92	1.0E+00	AA775191.1	EST_HUMAN	ac79808.s1 Stratiotes lung (#837210) Homo sapiens cDNA clone IMAGE:868791 3'
7802	20444	33349	1.49	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
7802	20444	33350	1.49	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8094	17734		1.28	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8291	20832	33753	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8291	20832	33754	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8413	20853		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8447	20887	33902	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8447	20887	33903	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M)
8475	24791		2.17	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT02228-18:1089-011-406 HT02229 Homo sapiens cDNA
8513	21052	33974	1.06	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8659	21198	34116	1.07	1.0E+00	M39427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9185	21712	34855	2.05	1.0E+00	BE807592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9402	21911	34880	1.34	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9402	21911	34881	1.34	1.0E+00	6753429	NT	Mus musculus chloride channel activated 1 (Clca1), mRNA
9428	22028	34987	2.08	1.0E+00	AV088554.1	EST_HUMAN	AV688554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9534	22034	34993	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9634	22034	34994	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9787	22265	35248	0.5	1.0E+00	X15468.1	NT	Human Coronavirus gene for membrane protein
9787	22265	35249	0.5	1.0E+00	X15468.1	NT	Human Coronavirus gene for membrane protein
10021	22516	35510	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHC8FB) mRNA
10021	22516	35511	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHC8FB) mRNA
10105	22800	35592	0.75	1.0E+00	A1077920.1	EST_HUMAN	015407.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10230	22725	35716	4.17	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW C04 5'
10372	22868	35959	18.78	1.0E+00	AA004982.1	EST_HUMAN	zh84a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10372	22868	35960	18.78	1.0E+00	AA004982.1	EST_HUMAN	zh84a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10404	22898	35983	0.93	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10853	23374	36393	1.87	1.0E+00	S90825.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt]
11587	18120	30527	1.57	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11837	24201		4.85	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12171	24410		3.08	1.0E+00	AW978184.1	EST_HUMAN	EST388283 IMAGE resequences, MAGN Homo sapiens cDNA
1618	14209	26742	0.97	9.8E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1618	14209	26743	0.97	9.8E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2684	15222	27784	1.17	9.8E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3665	16267		0.94	9.8E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5818	18440	31162	14.59	9.8E-01	P49857	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6029	18648	31389	0.83	9.8E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9185	21702		1.39	9.8E-01	U86667.1	NT	Lycopodium obscurum putative Mit1 copy 1 nematode-resistance gene
9474	21873		2.61	9.8E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10583	23128	36142	1.68	9.8E-01	AJ005029.1	NT	Danio rerio mRNA for Epi-like receptor tyrosine kinase rti8
549	13180	25658	1.77	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2338	14907		0.89	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2827	15379		2.05	9.8E-01	AF174844.1	NT	Xenopus laevis rec GTPase mRNA, complete cds
3869	18467	28630	0.95	9.8E-01	O87551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEONUCLEASE IV)
3872	18470	28633	0.61	9.8E-01	BE967439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3638461 3'
3872	18470	28634	0.61	9.8E-01	BE967439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3638461 3'
7250	19779	32634	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7250	19779	32635	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7641	20153	33038	1.13	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3860049 5'
7641	20153	33039	1.13	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3860049 5'
8653	21182	34110	0.77	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10334	22828		0.56	9.8E-01	AA825565.1	EST_HUMAN	cd55d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
10874	23395	36410	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
10874	23395	36411	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11587	24040	37109	1.78	9.8E-01	AI680876.1	EST_HUMAN	b42610.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
12058	24341		1.39	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT1), CDM protein (CDM), adrenolectomy protein >
7212	19743	32597	2.51	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8440	20880	33895	1.7	9.7E-01	AF149112.1	NT	Triticum aestivum shiwa rust resistance protein Yr10 (Yr10) gene, complete cds
8446	20886	33901	1.28	9.7E-01	AB0544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11048	23562		5.23	9.7E-01	BF511209.1	EST_HUMAN	UI-H-B14-act-e-07-Q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
12638	24728		2.92	9.7E-01	AL114281.1	NT	Borhylls chinese strain T4 cDNA library under conditions of nitrogen deprivation
4531	17115	29550	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucosylase (pgm1) mRNA, complete cds
4531	17115	29560	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucosylase (pgm1) mRNA, complete cds
4557	17140	29588	1.71	9.6E-01	AW769674.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5928	18550	31278	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2904
5928	18550	31277	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2904
8331	20872		1.23	9.6E-01	X95275.1	NT	P. taicaiarum complete gene map of plastid-like DNA (IR-A)
8785	21324	34248	0.47	9.6E-01	U81138.1	NT	Rattus norvegicus (strain R21) Rps27 gene, complete cds
9020	21557	34485	0.62	9.6E-01	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
10668	23481	36507	1.81	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11395	23847	36812	5.18	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG06 5'
11395	23847	36813	5.18	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG06 5'
11733	24138		2.36	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12388	24983	30609	2.8	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2515	15079	27851	1.02	9.5E-01	7705591	NT	Homo sapiens CG-125 protein (LOC31003), mRNA
2891	15248	27817	1.2	9.5E-01	Q02834	SWISSPROT	ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE I)
3850	16448	28909	1.89	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3850	16448	28910	1.89	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8831	21469	34387	0.63	9.5E-01	AI180162.1	EST_HUMAN	qd57d07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9034	21571	34500	1.07	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0285-241199-011-b02 CT0285 Homo sapiens cDNA
11123	23631	36874	1.71	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11326	23024	36033	1.69	9.5E-01	AW263789.1	EST_HUMAN	UI-H-B12-act-f-03-Q-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3235	15947		1.8	9.4E-01	AF165990.1	NT	Bartonella claridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3254	15888		2.47	9.4E-01	AF080585.1	NT	Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8789	21338	34265	0.88	9.4E-01	M90724.1	NT	Human Fe-gamma-receptor1A (FCGR2A) gene, exon 4
1789	14358		0.85	9.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5
2682	15220	27792	1.09	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4107	16701	29154	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4107	16701	29155	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	18403	31119	1.41	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5858	18481	31204	3.69	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
8011	20553	33456	1.62	9.3E-01	AA847040.1	EST_HUMAN	oe08b03.s1 NC1 CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1365357
8748	21267		1.13	9.3E-01	AF081981.1	NT	Xenopus laevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8867	21406	34330	1.01	9.3E-01	AL161634.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12508	24628	30893	1.87	9.3E-01	11440288	NT	Homo sapiens insulin 1,4,6-triphosphate receptor, type 2 (TIPR2), mRNA
12515	24634		2	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3278	15867	28369	3.99	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3816184 3'
5004	17577		0.92	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041383 5'
5894	18516		1.41	9.2E-01	7106410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30e4), mRNA
6140	18764	31512	4.4	9.2E-01	BF037588.1	EST_HUMAN	601461153F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3884061 5'
9578	22078	35042	1.31	9.2E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9683	22162	35135	1.15	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10168	22681	35656	3.47	9.2E-01	11430963	NT	Homo sapiens lysosomal aspartase-like protein 1 (LALP1), mRNA
10314	22808	35900	1.99	9.2E-01	BF583251.1	EST_HUMAN	7c58e08.x1 NC1 CGAP_Kid111 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW-NU5M_TRYBB
10526	23063	36074	1.75	9.2E-01	BE503811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
11568	24016	37085	2.27	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
							601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1688	14259	28783	4.89	9.1E-01	T86875.1	EST_HUMAN	ye52101.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121368 3' similar to contains
2169	14746		2.38	9.1E-01	8923056	NT	Alu repetitive element
							Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3239	15851	28331	0.93	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3239	15851	28332	0.93	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6315	18922	31699	1.42	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
8630	19226	32031	2.82	9.1E-01	G61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7577	20093	32970	15.96	9.1E-01	AA806623.1	EST_HUMAN	db71g08.s1 NC1 CGAP_G081 Homo sapiens cDNA clone IMAGE:1336862 3'
7718	20227	33115	3.12	9.1E-01	U72895.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12093	24978		33.14	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3241	15853	28335	0.81	9.0E-01	7681625	NT	Homo sapiens DKFP564M2423 protein (DKFP564M2423), mRNA
3401	18010		0.64	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4498	17054	28498	1.44	9.0E-01	AF089810.1	NT	Homo sapiens neuron III-alpha gene, partial cds

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7424	19048	32814	0.78	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7460	19074		1.84	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds
9271	21797	34748	0.54	9.0E-01	AF089761.1	NT	Danio rerio semaphorin Z1a mRNA, complete cds
9744	22242	35223	0.47	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 IV, no tag (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
5875	18497	31222	2.49	8.9E-01	AF026188.1	NT	Rabbit MHC fragment RLA-OF DNA
6308	18999		1.27	8.9E-01	X60988.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8152	20693		0.47	8.9E-01	AF260225.1	NT	Oithona nana cytochrome-c oxidase subunit 1 (cod) gene, partial cds; mitochondrial gene for mitochondrial product
8385	20905	33824	1.04	8.9E-01	AF256887.1	NT	Xyella fastidiosa, section 80 of 229 of the complete genome
11616	24058	37122	2.59	8.9E-01	AE003944.1	NT	Chlamydomonas reinhardtii, section 21 of 94 of the complete genome
11827	24202		5.33	8.9E-01	AE002186.2	NT	Chlamydomonas reinhardtii, section 21 of 94 of the complete genome
4840	17222	29678	2.1	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5578	18207	30658	0.7	8.8E-01	AF110617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
10960	23475	36500	3.82	8.8E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
11749	25087		2.27	8.8E-01	D80911.1	NT	Synochocystis sp. PCC8803 complete genome, 13/27, 1576593-1710643
480	13123	25609	1.48	8.7E-01	AF108953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2448	15013	27585	1.13	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF-1), mRNA
2898	15515	27884	5.67	8.7E-01	AA595883.1	EST_HUMAN	tr03f11.s1 NCJ CGAP Py4.1 Homo sapiens cDNA clone IMAGE:1076877
4845	17423	29875	0.61	8.7E-01	AF158539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
4845	17423	29878	0.61	8.7E-01	AF158539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
							Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzonate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzonate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put-
5151	17721		3.08	8.7E-01	AF121970.1	NT	RCAN00057-120500-013-007 NN0057 Homo sapiens cDNA
7883	20525	33431	0.66	8.7E-01	AW897335.1	EST_HUMAN	qf38a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
8860	21399	34322	0.75	8.7E-01	AI239458.1	EST_HUMAN	qf38a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
8860	21399	34323	0.75	8.7E-01	AI239458.1	EST_HUMAN	qf38a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
9853	22152	35122	1.7	8.7E-01	AE004983.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
10205	22700	35983	0.56	8.7E-01	BF570169.1	EST_HUMAN	802185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308908 3'
10205	22700	35984	0.56	8.7E-01	BF570169.1	EST_HUMAN	802185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308908 3'
10711	23239	36254	5.79	8.7E-01	BF363970.1	EST_HUMAN	QV6-NN1021-100800-337-003 NN1021 Homo sapiens cDNA
11582	24028	37097	4.31	8.7E-01	BF107694.1	EST_HUMAN	801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12146	24861		4.44	8.7E-01	AV681898.1	EST_HUMAN	AV681898 GLC Homo sapiens cDNA clone GLCGYG07 3'
500	13132		1.55	8.6E-01	X17012.1	NT	Rat IGF1 gene for insulin-like growth factor II
891	13505	26024	8.72	8.6E-01	W68089.1	EST_HUMAN	z444603.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343518 5'
2310	14882	27457	1.06	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3681	16282	28750	0.78	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3870	16468	28631	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6057	18674	31415	9.08	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6057	18674	31416	9.08	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6810	19401	32216	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6810	19401	32217	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7868	20410		1.33	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7986	20528	33434	0.54	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9603	22103		0.48	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12338	24812		1.73	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6826	19416	32232	1.32	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7533	20053	32928	2.38	8.5E-01	BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7932	20474	33383	0.51	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8357	20897	33817	0.84	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8357	20897	33818	0.84	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8441	20981	33806	0.51	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10252	22747	35734	1.38	8.5E-01	AB006798.1	NT	Cyanidium caldarium gene for SigC, complete cds
10252	22747	35735	1.38	8.5E-01	AB006798.1	NT	Cyanidium caldarium gene for SigC, complete cds
12077	24978		3.12	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12084	24355		7.82	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4882	17440	29880	0.82	8.4E-01	AF063975.2	NT	Fowl adenovirus 8, complete genome
5885	24747	30907	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5885	24747	30908	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
9868	22365		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
771	13390	25889	2.48	8.3E-01	M63437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3129	15743	28212	3.26	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3883	16481	28943	0.68	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4084	18680	29140	3.24	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5473	16107	30426	2.15	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9587	22087		3.14	8.3E-01	A1791852.1	EST_HUMAN	nr011212.6 NCI_CGAP_Ccd8 Homo sapiens cDNA clone IMAGE:1076485 5' similar to contains THR.H1 THR repetitive element:
10019	22514	35507	1.11	8.3E-01	AF098070.1	NT	Drosophila melanogaster L1s1 homolog mRNA, complete cds
10119	22814	35604	3.5	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10553	23089	36103	2.92	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10571	23106		2.52	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11183	23688	36735	2.45	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5
2098	14875	27244	3.23	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2137	14715		1.45	8.2E-01	AF145589.1	NT	Mus musculus trophoblast (Tm) gene, complete cds
3089	16567	29036	1.12	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4209	16798	29246	0.61	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL082w
4209	16798	29247	0.61	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL082w
5270	17832	30758	1.08	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5420	17977	30385	2.11	8.2E-01	AB028957.1	NT	Homo sapiens mRNA for KIAA1034 protein, partial cds
6871	19805	32439	0.8	8.2E-01	AJ010142.1	NT	Acanthamoeba muscaria mRNA for SCIII25 protein
6878	18554	32378	3.18	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081189-037-401 HT0243 Homo sapiens cDNA
7313	24778	32700	4.21	8.2E-01	Z12128.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
9838	22433	35409	0.63	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
9871	22468	35450	1.67	8.2E-01	AF052659.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
10123	22818	35909	0.59	8.2E-01	AF223988.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22818	35910	0.59	8.2E-01	AF223988.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10286	22781	35772	3.52	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10286	22781	35773	3.52	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11488	23947	37017	3.33	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11576	24022	37091	8.05	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11583	24029	37099	5.68	8.2E-01	H87398.1	EST_HUMAN	yr1402.1 Soares placenta, 820weeks_2N6HP869W Homo sapiens cDNA clone IMAGE:252185 5' similar to gb:U63072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12102	24364	30870	1.86	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2787	15340		1.78	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3504	16109	28585	2.99	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region
3504	16109	28588	2.98	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5048	17619		0.68	8.1E-01	AF202834.1	NT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6457	19058	31843	0.88	8.1E-01	U16780.1	NT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6735	19328	32134	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
6735	19328	32135	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
							Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
7852	20394	33298	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
7852	20394	33299	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8545	21084	34006	0.92	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8545	21084	34007	0.92	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
							XP01M03.X1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2882469 3' similar to SW1.YAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN; contains MER22.b1 PTR5 repetitive element
8705	21244	34167	1.08	8.1E-01	AW242847.1	EST_HUMAN	PROBABLE E4 PROTEIN
10032	22527	35522	0.54	8.1E-01	P08425	SWISSPROT	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11356	23810	36869	2.87	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11356	23810	36870	2.97	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11811	24183	31031	3.32	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 138 of the complete genome
188	12849		4.98	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphatase alkaline 15
310	12865	25453	7.95	8.0E-01	AJ132772.1	NT	Bos taurus tub and rat genes
2080	14661		1.47	8.0E-01	BF530982.1	EST_HUMAN	602072473F1 NC1 CGAP_Erm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3113	15728	28199	1.24	8.0E-01	AF127897.1	NT	Salmonella typhimurium diffractory receptor (SBO27) gene, partial cds
3354	15982	28439	1.13	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3766	16366		1.05	8.0E-01	AL102759.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4630	17213	29894	5.65	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5117	17689	30127	1.09	8.0E-01	7657352	NT	Mus musculus myosin D6 (Myo6), mRNA
7831	20473		2.32	8.0E-01	AW901488.1	EST_HUMAN	RCO-NN1012-270300-021-h08 NN1012 Homo sapiens cDNA
8462	21002	33919	1.17	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
479	13112	25602	1.37	7.9E-01	U11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
744	13384		1.05	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1648	14240		28.9	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
1695	14288		1.11	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2303	14876	27452	8.76	7.9E-01	AB004816.1	NT	Cryptosporidium parvum mRNA for mitsugumin29, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HIR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2304	14877	27453	5.48	7.8E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3567	16171	28653	2.33	7.8E-01	AF228684.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4389	18975		0.76	7.8E-01	BE263612.1	EST_HUMAN	601182033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4717	17268	26743	1.04	7.8E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4717	17268	26744	1.04	7.8E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5315	17877		5.8	7.8E-01	M28930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6485	19088	31888	0.69	7.8E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8053	20585	33502	2.62	7.8E-01	X90968.1	NT	P. sativum GR gene
9466	21861	34948	4.57	7.8E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vegG3M-B) mRNA, partial cds
9862	22457	35440	4.27	7.8E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10003	22408	35487	0.75	7.8E-01	AV700860.1	EST_HUMAN	AV700860 GK Homo sapiens cDNA clone GKCDRE12 3'
10405	22859	35694	0.71	7.8E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10866	23407		2.28	7.8E-01	7682471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11089	23801	38639	2.72	7.8E-01	P16022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
909	13522		1.4	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2314	14888	27461	14	7.8E-01	AW955667.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4811	17389	28940	0.81	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5189	17754		0.81	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6219	18828	31803	2.33	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6367	18971	31750	1.05	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6589	19168	31888	0.75	7.8E-01	AL445068.1	NT	Thermoplasma acidophilum complete genome; segment 4/6
8428	20688	33881	1.04	7.8E-01	BF109627.1	EST_HUMAN	754405.1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
8160	21695	34639	1.02	7.8E-01	Y10159.1	NT	D. discoideum racGAP gene
9255	21781	34733	0.53	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAN) (NUP214), mRNA
10031	22528		0.78	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12071	24657		2.33	7.8E-01	L23260.1	NT	Arabidopsis thaliana 1-aminino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
150	12813	25300	4.65	7.7E-01	AF184345.1	NT	Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
755	13374		1.44	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aalpha) and major histocompatibility protein class II beta chain (Ibeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like
2737	15292	27860	2.33	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3400	16009		0.82	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosaminopolypeptide N-acetylglucosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
3660	16262	28734	4.78	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4488	17071	28521	3.17	7.7E-01	AF189488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4488	17071	28522	3.17	7.7E-01	AF189488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5749	18375	31084	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5749	18375	31085	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6110	18726	31478	0.8	7.7E-01	R08600.1	EST_HUMAN	Y724502 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
9758	22256	35239	0.82	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
11957	24280		15.01	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
4790	17370	29822	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
4790	17370	29823	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
6248	18857	31628	4.91	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6248	18857	31628	4.91	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6641	19237	32039	0.7	7.6E-01	P37838	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA 24
6935	18043	30465	0.95	7.5E-01	A1253399.1	EST_HUMAN	seq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6935	18043	30488	0.95	7.5E-01	A1253399.1	EST_HUMAN	seq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7113	19453	32269	0.98	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8009	20551	33455	1.34	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; Phtp (Tph) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pht27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8068	20610	33522	1.76	7.6E-01	6857752	NT	Mus musculus adinin (Adinl-pending), mRNA
8068	20610	33523	1.76	7.6E-01	6857752	NT	Mus musculus adinin (Adinl-pending), mRNA
8267	20808	33727	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8267	20808	33728	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8897	21435	34359	0.91	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9203	21720	34694	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9203	21720	34695	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11236	23767	36824	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11236	23767	36825	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11566	24004		5.74	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11711	24121		6.31	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
539	13170		1.32	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
610	13238	25712	1.13	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7530	20050	32823	0.74	7.6E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (epb) mRNA, complete cds
12027	24918		5.26	7.5E-01	AF169151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12522	24638	30897	1.91	7.5E-01	D00007.1	NT	Synschoeculus sp. PCC6803 complete genome, 9/27, 1058467-1188865
1169	13771	26279	1.36	7.4E-01	AI588148.1	EST_HUMAN	Int14b09.x1 NCJ_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2187577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
3789	16369	28854	0.93	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4400	16885	29430	7.7	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7785	20328	33234	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7785	20328	33235	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8568	21107	34026	0.93	7.4E-01	BF346268.1	EST_HUMAN	602018456F1 NCJ_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8647	21186		0.64	7.4E-01	U87860.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9026	21563	34492	7.17	7.4E-01	BE747503.1	EST_HUMAN	601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9083	21619	34554	1.19	7.4E-01	AA187866.1	EST_HUMAN	zp67h01.s1 Strabegene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625287 3' similar to SW:TCPO_MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10301	22795	35786	0.59	7.4E-01	11424833	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11518	23964	37034	1.68	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11518	23964	37035	1.68	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11677	24096		4.11	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
11784	24176		1.28	7.4E-01	AI472841.1	EST_HUMAN	Int13h01.x1 NCJ_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043385 3'
4723	17304	28748	0.72	7.3E-01	AE001168.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4810	17388	28839	2.93	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5260	17623	39248	0.89	7.3E-01	Q43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6720	16314	32116	5.86	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6720	16314	32117	5.86	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7151	24777	32525	0.82	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7549	20068	32942	7.77	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7549	20068	32943	7.77	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11307	23800	36859	3.86	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11307	23800	36880	3.86	7.3E-01	AA678019.1	EST_HUMAN	z25508.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431788 3'
884	13479		1.86	7.2E-01	U29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2000	14582	27141	3.04	7.2E-01	X79140.1	NT	N. tabacum Nelf-4A13 mRNA
2501	15065	27639	1.36	7.2E-01	AB003605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3103	15718	28188	1.29	7.2E-01	AF188100.1	NT	Footpox virus, complete genome
3500	16105	28580	2.97	7.2E-01	AF065906.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3040	16538	20005	1.81	7.2E-01	BF338350.1	EST_HUMAN	002035589F1 NC1 CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4185	16775	29222	0.6	7.2E-01	U02588.1	NT	Diclyocaulus viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds
4884	17459	28911	2.54	7.2E-01	D80314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5348	17908	30323	0.9	7.2E-01	AF158800.2	NT	Streptococcus thermophilus bacteriophage Sfi11, complete genome
5388	17945	30358	0.69	7.2E-01	AL181583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7265	19783	32649	0.82	7.2E-01	U68633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8301	20931	33851	1.15	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
8893	21431		0.53	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10243	22738	35729	2.14	7.2E-01	BF70061.1	EST_HUMAN	602118381F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4275381 5'
10618	23150	36182	5.23	7.2E-01	U62623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12037	18775	29222	1.86	7.2E-01	U02588.1	NT	Diclyocaulus viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds
12233	24449		4.42	7.2E-01	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
12266	24995		1.67	7.2E-01	Y10168.1	NT	B. thuringiensis PK1 & cap genes, putative
721	13341	25831	10.56	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3098	15713	28185	18.71	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4287	16873	29321	4.11	7.1E-01	7305360	NT	Mus musculus obogelin (Otog), mRNA
4287	16873	29322	4.11	7.1E-01	7305360	NT	Mus musculus obogelin (Otog), mRNA
6103	18719	31471	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6103	18719	31472	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7029	19563	32360	6.04	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltryptophan synthase (pr) gene, complete cds
8132	20673	33584	0.53	7.1E-01	H54244.1	EST_HUMAN	y98009.s1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:202981 3'
8671	21210	34128	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-B10567-301289-011-009 BT0567 Homo sapiens cDNA
8671	21210	34129	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-B10567-301289-011-009 BT0567 Homo sapiens cDNA
9769	22867	35252	1.48	7.1E-01	BE004405.1	EST_HUMAN	601498330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10309	22803	35795	1.08	7.1E-01	M12961.1	NT	Human T-cell receptor gamma-chain J2 gene
12012	24878		2.58	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1272	13988	26387	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
1272	13988	26388	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
2482	15057	27630	1.22	7.0E-01	NC2412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerobels_2NbrHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2482	15057	27631	1.22	7.0E-01	NC2412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerobels_2NbrHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5213	17778		1.98	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5362	17922	30336	2.99	7.0E-01	AE003921.1	NT	Xylella fastidiosa, section 87 of 228 of the complete genome
6107	18723		1.03	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8319	20800		11.92	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9240	21766	34714	0.61	7.0E-01	U53988.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds
9240	21766	34715	0.61	7.0E-01	U53988.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds
10899	23513	36546	1.99	7.0E-01	AV763942.1	EST_HUMAN	AV763942 MDS Homo sapiens cDNA clone MDSCH04 5'
10899	23513	36547	1.98	7.0E-01	AV763942.1	EST_HUMAN	AV763942 MDS Homo sapiens cDNA clone MDSCH04 5'
12584	24918	30715	1.35	7.0E-01	8630484	NT	Bacteriophage N15 virion, complete genome
1005	13616	26130	10.2	6.9E-01	U68674.1	NT	Candida albicans equulene epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds
1005	13616	26131	10.2	6.9E-01	U68674.1	NT	Candida albicans equulene epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds
1353	13948	28472	2.8	6.9E-01	AA503530.1	EST_HUMAN	nm28e09.s1 NCI_OGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3256	15868	28348	1.7	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5654	18576	31310	0.8	6.9E-01	AB035982.1	NT	Branchiostoma belcheri BbNA3 mRNA for nucleohistone actin, complete cds
6508	10108	31803	1.31	6.9E-01	BE266188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7821	20483	33368	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7921	20483	33370	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8098	21634		0.83	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9611	22111	35073	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9611	22111	35074	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10307	22801	35793	0.66	6.9E-01	BF242367.1	EST_HUMAN	601880580F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4108419 5'
11138	23646	36687	1.94	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11138	23646	36688	1.94	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11661	24870		2.38	6.9E-01	Q69958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK
12670	25003	30811	1.33	6.9E-01	A1886312.1	EST_HUMAN	HEAD PROTEIN 1) (MFT-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)
992	13604	28118	1.28	6.9E-01	AF017784.1	NT	wn3102.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2447067 3'
2698	15266		1.25	6.9E-01	D90917.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2858	14249	28783	1.62	6.9E-01	AA854475.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
4872	17264	28706	1.45	6.9E-01	J00782.1	NT	af75a06.a1 Soares parathyroid tumor_NHHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to
8556	22058	35017	2.11	6.9E-01	AB037766.1	NT	gb:X58411_mal1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
10281	22756		0.48	6.9E-01	AA687838.1	EST_HUMAN	Rat(hooded) prolactin gene: exon III and flanks
10965	23480	36505	2.86	6.9E-01	AJ276875.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10965	23480	36508	2.86	6.9E-01	AJ276875.1	NT	hnt13e07.a1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_mal1
10983	23507	36540	2.16	6.9E-01	AF038939.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
10983	23507	36541	2.16	6.9E-01	AF038939.1	NT	Stagonospora avenae bg1 gene for beta-glucosidase, exons 1-4
11178	23884	36730	2.2	6.9E-01	AF184151.1	NT	Stagonospora avenae bg1 gene for beta-glucosidase, exons 1-4
11475	23925	36895	1.77	6.9E-01	AF110520.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11475	23925	36898	1.77	6.9E-01	AF110520.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
320	12074	25463	27.63	6.7E-01	AF213884.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
361	13010	25463	28.51	6.7E-01	AF213884.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28,
1955	14539		0.97	6.7E-01	M12132.1	NT	KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
2192	14768	27340	1.85	6.7E-01	AA451864.1	EST_HUMAN	RPS18 genes, complete cds; Secm21 gene, partial>
2211	15460	27361	2.68	6.7E-01	AF188073.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete
3026	15942	28120	4.28	6.7E-01	6878580	NT	cds
4550	17133	28581	0.64	6.7E-01	X74421.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete
							cds
							Quail fast skeletal muscle troponin I gene, complete cds
							zx12g12.s1 Soares total_fetus_Nb27IF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to
							contains element TAR1 repetitive element:
							Drosophila melanogaster Msl85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds,
							alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
							Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
							S.tuberosum mRNA for glucose-6-phosphatase dehydrogenase

Table 4

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5100	17672	30111	0.96	6.7E-01	AW079110.1	EST_HUMAN	xs89g12.x1 NCL CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
5700	18328	30829	0.8	6.7E-01	J04838.1	NT	M.barkei ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5700	18328	30830	0.8	6.7E-01	J04838.1	NT	M.barkei ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6116	18732	31485	0.83	6.7E-01	AE001488.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6465	19068	31851	1.55	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6465	19068	31852	1.55	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
7358	19882		4.12	6.7E-01	AE004808.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7378	19904	32768	0.9	6.7E-01	AE004808.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10049	22544		0.87	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10832	23553	36368	2.52	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0708-010800-197-c03 HT0769 Homo sapiens cDNA
11333	23031	36040	3.45	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2546	15110	27682	2.68	6.6E-01	AF075240.1	NT	Homo sapiens SLT1 protein (SLT2) mRNA, partial cds
2724	15279	27846	1.01	6.6E-01	AF199330.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3536	16141	28623	1.35	6.6E-01	4506890	NT	Homo sapiens same domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sarnaphorin) 5A (SEMA5A) mRNA
3719	16320	28788	3.42	6.6E-01	Y07698.1	NT	C.albicans random DNA marker, 282bp
4187	16777			6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
5227	17791	30210	0.97	6.6E-01	AI218230.1	EST_HUMAN	q23a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845488 3' similar to contains PTR5.b2 MER28 repetitive element:
6474	18075	31858	4.22	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7675	20188	33074	3.61	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
8501	21040	33981	0.64	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
8582	22082		1.73	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8915	22411		0.68	6.6E-01	AU118198.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
12118	24377	30973	1.27	6.6E-01	AF110001.1	NT	Homo sapiens guanylate cyclase activating protein 3 (GCAP3) gene, exon 4 and complete cds
651	13274	25751	1.12	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
651	13274	25752	1.12	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3480	16086	28560	5.04	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4110	16704	29157	1.1	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4368	16856	28398	3.29	6.5E-01	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4699	17261	29728	1.28	6.5E-01	D00584.1	NT	Oryza sativa gene for prepro-glutelin, exons 1, 2, 3, 4, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	17784	30202	2.39	6.5E-01	U28021.1	NT	Phascolus vulgaris ATPase gamma subunit mRNA, nuclear genes encoding mitochondrial protein, partial cds
5336	17897	30312	1.02	6.5E-01	Z70628.1	NT	H.sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71)
6825	19415	32231	1.26	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosome matrix protein, complete cds
7663	20176	33062	0.96	6.5E-01	A1799882.1	EST_HUMAN	wc46a02.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2321642 3'
9751	22249		1.25	6.5E-01	T78904.1	EST_HUMAN	yc21b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108847 3'
10238	22733	35725	2.49	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10512	23050	36061	3.35	6.5E-01	H87583.1	EST_HUMAN	yw1706.r1 Soares placenta_8to9weeks_2NdrHP8b9W Homo sapiens cDNA clone IMAGE:252515 5'
10566	23102	36116	4.35	6.5E-01	AA601287.1	EST_HUMAN	nc15c07.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10669	23201		4.29	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11470	23920	36968	2.7	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12067	24348		8.24	6.5E-01	BE485050.1	EST_HUMAN	hiv74a10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12321	24817		3.04	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
273	12930	25417	9.34	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3502	16107	28583	3.78	6.4E-01	U48854.2	NT	Mus musculus dyroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3928	16526	28663	1.33	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4591	17174	28619	0.66	6.4E-01	Y12488.1	NT	M.musculus wtn gene
4591	17174	28620	0.66	6.4E-01	Y12488.1	NT	M.musculus wtn gene
5402	17960	30371	0.97	6.4E-01	AE002551.2	NT	Neisseria meningitidis serogroup B strain MC58 section 183 of 208 of the complete genome
8549	21088	34010	1.76	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10001	22496	35486	8.26	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10015	22510	35501	1.16	6.4E-01	BF670405.1	EST_HUMAN	602150288F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
12188	24420		29.97	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCC09 5'
459	13093	25587	3.75	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
560	13191	25669	58.3	6.3E-01	U32686.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2207	14763	27356	3.24	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2614	15176	27744	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2614	15176	27745	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3050	15668		0.76	6.3E-01	Y17275.1	NT	Lycopodium obscurum p80a gene, complete CDS
6214	18624	31595	0.78	6.3E-01	BE083808.1	EST_HUMAN	PMO-B10757-010500-002-a05 BT0757 Homo sapiens cDNA
6712	19306	32110	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds
6712	19306	32111	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (msg) gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8458	20908		3.32	6.3E-01	BE02044.1	EST_HUMAN	601676888F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956351 5'
8819	21358	34284	0.81	6.3E-01	S62927.1	NT	glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9147	21682	34627	1.15	6.3E-01	BF216884.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5'
9341	21855	34804	2.9	6.3E-01	0827521	NT	Varicella virus, complete genome
9341	21855	34805	2.9	6.3E-01	0827521	NT	Varicella virus, complete genome
9851	22349		0.67	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 69 of 95 of the complete genome
10324	22818	35814	1.52	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR216w
10421	22916	35916	0.87	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10839	23456	36479	2.45	6.3E-01	AA977715.1	EST_HUMAN	tr08h08.at NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002816 HLARK.
11216	23719	36773	15.21	6.3E-01	A1804160.1	EST_HUMAN	CM-BT043-080298-046 BT043 Homo sapiens cDNA
11302	23795	36853	1.94	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11458	23808	36875	2.02	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11769	25042	30505	30.63	6.3E-01	0810283	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
11884	24219		1.85	6.3E-01	AF106227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
12082	24953		3.2	6.3E-01	X63528.1	NT	Glimicole pscD gene
5175	17742	30171	0.71	6.2E-01	AF157898.1	NT	Spermophilus suslicus isolate S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
6030	18049	31390	2.03	6.2E-01	Q10195	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7506	20028		3.14	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Carr-rs4) mRNA, partial cds
7548	24786	32941	1.08	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magee8 gene, Celltractin, NAD(P) sterol dehydrogenase and Zinc finger protein 185
8243	20784	33703	5.65	6.2E-01	H72255.1	EST_HUMAN	ys01608.at Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
8780	21329	34254	0.54	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9370	20308	33212	1.75	6.2E-01	BE562687.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3660010 5'
9429	21938		2.35	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
9880	22485	35472	5.85	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10428	22923	35927	3.76	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL
10429	22923	35928	3.76	6.2E-01	P27410	SWISSPROT	PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2438	15005		4.95	6.1E-01	6878076	NT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL
4632	17215	28688	1.05	6.1E-01	4557538	NT	PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
							Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
							Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6141	17712	30142	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxydiphenylbenzoate methyltransferase mRNA, complete cds
5141	17712	30143	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxydiphenylbenzoate methyltransferase mRNA, complete cds
5727	18353	31057	1.34	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CehMyd (nhr-1) alternatively spliced genes, complete cds
6951	19528	32351	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6951	19528	32352	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
8175	20716	33632	3.57	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8730	21269	34187	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase 4 (MAP4K4), mRNA
8730	21269	34188	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase 4 (MAP4K4), mRNA
8338	21850	34798	19.4	6.1E-01	AF238117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
8338	21850	34799	19.4	6.1E-01	AF238117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9756	22254	35238	1.15	6.1E-01	AE004462.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
8959	22454	35436	1.8	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC8A3) gene, complete cds
10837	23358		8.53	6.1E-01	X74507.1	NT	P. sativum mdh mRNA for chloroplast malate dehydrogenase (NADP+)
11581	24027	37095	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11581	24027	37098	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12530	24643		1.91	6.1E-01	X95287.1	NT	M.mazaei orfA, orfB, and orfC of archaeal ABC-transporter system
520	13152	25635	1.46	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
587	13217		3.41	6.0E-01	5802889	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLAS2), mRNA
1496	13999	26528	1.93	6.0E-01	AF066263.1	NT	Human respiratory syncytial virus strain CH89-53b attachment protein (G) gene, complete cds
3887	16485	28946	0.88	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4267	18853		1.16	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5485	18118	30528	1.93	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5631	18280	30732	2.28	6.0E-01	AW139713.1	EST_HUMAN	UHLB1-eeb-a-10-0-UJ.s1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718819 3'
6660	19256	32059	3.73	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6787	19360	32189	0.79	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7391	19816	32780	5.29	6.0E-01	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, even 1
8066	20608	33520	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8066	20608	33521	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9737	22235	35214	2.22	6.0E-01	AB008183.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10174	22688		1.61	6.0E-01	Q01487	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10638	23453	38478	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10638	23453	38477	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11428	23877	38842	2.84	6.0E-01	A420823.1	EST_HUMAN	U0807.01 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2086821 3'
12158	24398	30878	1.82	6.0E-01	11421883	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12285	24475		1.88	6.0E-01	AA708087.1	EST_HUMAN	388805.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone IMAGE:482778 3'
12428	24879		1.29	6.0E-01	5803138	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12469	24885	30709	2.49	6.0E-01	0055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12489	24810		6.82	6.0E-01	BE157817.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1038	13848	28160	1.08	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1447	14039	28568	1.08	5.9E-01	6880232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3308	15919	28395	5.12	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3308	15919	28396	5.12	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4304	16890		4.32	5.9E-01	AF162756.1	NT	Rattus norvegicus ceroidin 2 mRNA, partial cds
6591	19188	31981	1.48	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP-2) gene, exon 1 and partial cds
7310	19838	32896	5.58	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7841	20483	33395	0.57	5.9E-01	D90911.1	NT	Synschoecia sp. PCC6803 complete genome, 13/27, 1576593-1718843
9462	21987	34943	0.83	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds
9827	22325		0.68	5.9E-01	P08483	SWISSPROT	E6 PROTEIN
10091	22586	35579	1.15	5.9E-01	P56284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10551	23087	36102	3.24	5.9E-01	Q9X015	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10557	23083	36105	1.75	5.9E-01	AF187944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10840	23381	36378	3	5.9E-01	AW837176.1	EST_HUMAN	PM1-DT0041-190100-002-H03 DT0041 Homo sapiens cDNA
11073	23585	36828	2.25	5.9E-01	AF064608.1	NT	Mus musculus strain SPRET/EJ CD48 antigen (C448) gene, partial cds
11810	24182	31030	1.92	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12053	24336		2.88	5.9E-01	AB017706.1	NT	Aspergillus cryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12280	24483		7.56	5.9E-01	P34828	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1852	14536	27082	1.8	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4058	16853	28119	1.22	5.8E-01	BF685738.1	EST_HUMAN	60185247AF1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078131 5'
4612	17186	28641	3.73	5.8E-01	AB008077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4814	17489		1.18	5.8E-01	AF110846.1	NT	Megascella scalaris sac-lethal homolog (Megsd) gene, partial cds, alternatively spliced products
5577	18208		0.75	5.8E-01	AE002182.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5722	18348	31051	2.52	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6331	18937	31713	2.37	6.8E-01	D78659.1	EST_HUMAN	HUM500E088 Human placenta polyA+ (TFujihara) Homo sapiens cDNA clone GEN-600E08 5'
6454	19055	31840	0.71	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
6903	19637		2.47	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7628	20370		2.57	5.8E-01	H41571.1	EST_HUMAN	Yn81b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
8031	20573	33477	0.66	5.8E-01	A1280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8031	20573	33478	0.66	5.8E-01	A1280051.1	EST_HUMAN	qf85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8131	20672	33582	2.34	5.8E-01	P14328	SWISSPROT	qf85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8131	20672	33583	2.34	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP08
8823	21362	34287	9.48	5.8E-01	AJ270774.1	NT	SPORE COAT PROTEIN SP08
8802	21440	34363	0.88	5.8E-01	Q27368	SWISSPROT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 9-11
8903	21441	34364	0.96	5.8E-01	Q20471	SWISSPROT	TRANSCRIPTION FACTOR E2F
9514	22014		0.89	5.8E-01	BF031606.1	EST_HUMAN	PUTATIVE CASEIN KINASE I F48F2.2 IN CHROMOSOME X
10869	23380	38405	9.44	5.8E-01	AJ243213.1	NT	P01557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5'
10915	23434		3.66	5.8E-01	BF700082.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11021	23535		2.04	5.8E-01	BF700082.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3078	15694		0.86	5.7E-01	6766253	NT	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3260	15872	28352	1.58	5.7E-01	Q9W1J2	SWISSPROT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3552	16156		2.63	5.7E-01	AB033503.1	NT	Populus euphratica peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3973	16571	28041	3.09	5.7E-01	AF011591.1	NT	Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds
8498	19097	31881	3.67	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6812	19403	32219	0.72	5.7E-01	AA194201.1	EST_HUMAN	z338c08.r1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:685674 5'
6945	18053	30478	1.26	5.7E-01	AL111440.1	NT	Bethyis chinensis strain T4 cDNA library under conditions of nitrogen deprivation
7741	20249	33142	1.97	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR)(P5C REDUCTASE)
7911	20453		0.57	5.7E-01	AJ251835.1	NT	Mus musculus Kcrq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
9715	22213	35186	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9715	22213	35187	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10468	22662	35973	0.86	5.7E-01	BF540982.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068810 5'
3410	16019	28498	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3410	16019	28499	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4324	16910	28351	0.89	5.6E-01	D83135.1	NT	Chicken TBP gene, second, complete cds
8738	21277	34200	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCF5R05 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8738	21277	34201	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKX Homo sapiens cDNA clone GKCF5F05 5'
9297	21897	34844	1.11	6.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11658	24085		2.5	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11779	24168	36775	1.28	5.6E-01	AA493535.1	EST_HUMAN	1075910.s1 NCI_CGAP_P6 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element:
12156	18028	30480	3.31	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12185	24419		2.58	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12619	24698		3.11	5.6E-01	BF573828.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1253	13650	26367	1.13	5.5E-01	8383912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (PcoB), mRNA
2725	15280	27847	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2725	15280	27848	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2843	15559	28033	0.69	5.5E-01	5902085	NT	Homo sapiens superkiller virilicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3102	15717		1.51	5.5E-01	H46219.1	EST_HUMAN	Y018a10.s1 Soares adult brain N2b5tHB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3271	15883	28365	2.68	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3755	16356	28825	0.97	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
8388	20928	33846	0.68	5.5E-01	A1791768.1	EST_HUMAN	cr2b01.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9882	22161		0.74	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10279	22774	35763	0.84	5.5E-01	T05047.1	EST_HUMAN	EST02835 Fetal brain, Strabagene (cat#836208) Homo sapiens cDNA clone HFBCQ35
151	12814	25301	12.97	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
161	12814	25302	12.97	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
611	13239	25713	1.6	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
611	13239	25714	1.6	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1314	13908	28428	2.58	5.4E-01	AW886087.1	EST_HUMAN	QV4-NIN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2154	14731		3.6	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2298	14870	27446	2.18	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
3384	16582	28053	0.62	5.4E-01	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
6259	17822		1.04	5.4E-01	AW747872.1	EST_HUMAN	QV0-BT0041-061088-033-c02 BT0041 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5388	13239	25713	0.59	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AwE (awE), <i>HrpW</i> (hrpW), and <i>GstA</i> (gstA) genes, complete cds; and unknown genes
5388	13239	25714	0.59	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AwE (awE), <i>HrpW</i> (hrpW), and <i>GstA</i> (gstA) genes, complete cds; and unknown genes
5838	18482	31185	0.81	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6338	18944	31723	1.49	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
7084	18685	32504	1.1	5.4E-01	BE98582.2	EST_HUMAN	607680278R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:38060890 3'
7374	18900	32762	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7374	18900	32763	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
							MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
7378	19902	32766	1.47	5.4E-01	Q84428	SWISSPROT	602076545F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243680 5'
9801	22398		1.98	6.4E-01	BF572636.1	EST_HUMAN	NITRATE REDUCTASE [NADPH] (NIR)
10957	23472	38497	3.25	5.4E-01	P38858	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11485	23934	37004	5.79	5.4E-01	Q80875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11485	23934	37005	5.79	5.4E-01	Q80875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11586	18944	31723	2.42	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
11725	24132		2.52	5.4E-01	A1858368.1	EST_HUMAN	w437g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
							Homo sapiens HLA class III region containing tensin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, hepcase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes.?
542	13173	25683	2.28	5.3E-01	AF019413.1	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2811	15363	27881	6.51	5.3E-01	4506328	NT	Homo sapiens secreted C-type lectin precursor (LSL CL) gene, complete cds
2811	15363	27882	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3280	15861	28370	3.13	5.3E-01	AF087658.1	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
4280	16876		1.39	5.3E-01	U39887.1	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
5649	18277	30753	1.91	5.3E-01	A1820821.1	EST_HUMAN	Myeloplasma genitalium section 9 of 51 of the complete genome
5649	18277	30754	1.91	5.3E-01	A1820821.1	EST_HUMAN	z142h12.j6 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740711 5'
5742	18388	31075	0.87	5.3E-01	AA183872.1	EST_HUMAN	z142g09.f1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:688112 5'
5742	18388	31076	0.87	5.3E-01	AA183872.1	EST_HUMAN	z142g09.f1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:688112 5'
							7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5827	18451	31174	1.84	5.3E-01	BE645620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5827	18451	31175	1.84	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8835	21374		1.83	5.3E-01	L01950.2	NT	Ribulose biphosphate carboxylase (rbcl.) gene, partial cds; chloroplast gene for chloroplast product
8885	21423	34348	0.63	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NC1_CGAP_L124 Homo sapiens cDNA clone IMAGE:3 similar to contains element MER29 repetitive element:
8885	21423	34349	0.63	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NC1_CGAP_L124 Homo sapiens cDNA clone IMAGE:3 similar to contains element MER29 repetitive element:
10112	22807	35597	0.48	5.3E-01	A054210.1	EST_HUMAN	w94h02.x1 NC1_CGAP_Met15 Homo sapiens cDNA clone IMAGE:2561275 3' similar to SW-COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR:
11435	23885	36952	6.92	5.3E-01	BE566281.1	EST_HUMAN	601339887F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3692188 5'
11650	24881		4.22	5.3E-01	A0918053.1	EST_HUMAN	cg30a05.s1 NC1_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441378 3' similar to gb:J02811 APOLIPROTEIN D PRECURSOR (HUMAN);
849	13465	25973	19.16	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1208	13808	28319	10.07	5.2E-01	Q8WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1233	13832	26348	2.91	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1830	14514		4.11	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2191	14767	27339	2.97	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3163	15767	28233	1.67	5.2E-01	U65942.1	NT	Chlamydomonas abortus strain S203 POMF91A and POMF90A precursor, genes, complete cds
3274	15888		0.71	5.2E-01	D73443.1	NT	Azotobacter vinelandii lcl gene for isocitrate dehydrogenase, complete cds
3452	16059		1.74	5.2E-01	AL116780.1	NT	Bovine cDNA library under conditions of nitrogen deprivation
3462	16097	28572	2.49	5.2E-01	AA884165.1	EST_HUMAN	am77g05.s1 Strabegene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3694	16285		0.92	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5161	17730		0.87	5.2E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (VHL), mRNA
5314	17878		0.89	5.2E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5834	18458	31179	0.97	5.2E-01	AA284281.1	EST_HUMAN	z044409.T7 Saccharomyces cerevisiae NthSF Homo sapiens cDNA clone IMAGE:325160 3'
9046	24795	35115	1.19	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9046	24795	35116	1.19	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9845	22343	35325	0.64	5.2E-01	AA194518.1	EST_HUMAN	z050509.J1 Strabegene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
9840	22435	35411	1.65	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12580	24682		4.94	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
645	13288	25748	2.13	5.1E-01	M59509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
676	13300	25781	3.98	5.1E-01	AJ233944.1	NT	Polypodium vitellinum (strain P1 v1) 16S rRNA gene

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
676	13300	25782	3.98	5.1E-01	AJ233944.1	NT	Polyomavirus (strain PI v1) 16S rRNA gene
1682	14284		0.88	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
2069	14949		11.33	5.1E-01	BF683095.1	EST_HUMAN	602139319F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4288117 5'
4151	16743	29197	4.61	5.1E-01	A1858495.1	EST_HUMAN	W39b12.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2427283 3'
4268	16852	28300	3.03	5.1E-01	P66380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5229	17763		0.71	5.1E-01	BE091798.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6422	19025		0.79	5.1E-01	AV712328.1	EST_HUMAN	AV712328 DCA Homo sapiens cDNA clone DCAALU07 5'
6897	19495	32316	1.42	5.1E-01	R80873.1	EST_HUMAN	y64e09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8507	21046	33068	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-601 ST0023 Homo sapiens cDNA
8507	21046	33067	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-601 ST0023 Homo sapiens cDNA
9602	22102	35065	4.6	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9605	22105	35068	3.4	5.1E-01	W22302.1	EST_HUMAN	6581 Human retina cDNA Tap5091-cleaved sublibrary Homo sapiens cDNA not directional
10065	22580	35555	0.95	5.1E-01	M84579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
11874	24805		2.04	5.1E-01	BF030207.1	EST_HUMAN	60155883F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3826767 5'
12128	24385		2.01	5.1E-01	BF439882.1	EST_HUMAN	nuc-511f10.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3408218 3' similar to contains element
2180	14757	27328	1.4	5.0E-01	4885552	NT	TAR1 repetitive element ;
2180	14757	27327	1.4	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2189	14785	27335	5.46	5.0E-01	AF008210.1	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2189	14785	27336	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHIFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3740	16341	28809	5.58	5.0E-01	AE001785.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHIFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3811	16410	28875	0.65	5.0E-01	U55574.1	NT	Thermococcus maritima section 97 of 136 of the complete genome
3942	16540	29008	3.11	5.0E-01	AB033010.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
8497	21007		1.78	5.0E-01	M82304.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
8604	21143	34057	0.64	5.0E-01	BF107848.1	EST_HUMAN	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8379	20318	33219	3.1	5.0E-01	BF317212.1	EST_HUMAN	60182350R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9543	22043	35004	1.34	5.0E-01	P35573	SWISSPROT	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE] (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9543	22043	35005	1.34	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHIER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10291	22788		1.04	5.0E-01	BE88218.1	EST_HUMAN	601445024F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849438 5'
11815	24187		3.45	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12554	24856		2.38	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12569	24868		4.27	5.0E-01	O13881	SWISSPROT	NUCLEAR ENVELOPE PROTEIN OUT11
822	13439	26948	2.31	4.9E-01	BF571482.1	EST_HUMAN	602076849F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4243860 5'
1688	14282	26827	1.6	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1949	14533	27089	1.35	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5602	18231	30681	1.32	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6187	18797	31585	2.35	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6187	18797	31566	2.35	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7475	18997	32882	1.9	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8920	21458		1.49	4.9E-01	BF209791.1	EST_HUMAN	601874984F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4102503 5'
9115	21651	34592	0.96	4.8E-01	AW339905.1	EST_HUMAN	h90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907288 3' similar to TR:095714
9220	25126		2.2	4.8E-01	10948883	NT	O95714 HERC2 ;
10220	22715	35708	0.74	4.8E-01	AF053880.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
11704	24117		2.48	4.8E-01	AF178912.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12548	25081		5.73	4.9E-01	AA813562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12555	24657	30872	1.74	4.9E-01	AL163301.2	NT	h922811.s1 NCI_CGAP_C010 Homo sapiens cDNA clone IMAGE:1144652 3'
12630	24708		1.36	4.8E-01	11431438	NT	Homo sapiens chromosome 21 segment HS21C101
3591	16195		1.05	4.8E-01	AA012842.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4782	17011		0.62	4.8E-01	4504850	NT	cd32a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
5688	18324	30827	8.6	4.8E-01	J02987.1	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
6790	18381		4.22	4.8E-01	AA655878.1	EST_HUMAN	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
7357	18883		1.85	4.8E-01	5031650	NT	nu85f09.s1 NCI_CGAP_AM1 Homo sapiens cDNA clone IMAGE:1217513
7682	20174	33061	0.87	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (DS2288E) mRNA
7738	20246	33138	3.72	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
7738	20246	33139	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7846	20388	33281	1.36	4.8E-01	A1820744.1	EST_HUMAN	y77110.y6 Soares breast 2NH1Bst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element
9169	21746		1.13	4.8E-01	BE155148.1	EST_HUMAN	MER8 repetitive element:
9821	22417		0.58	4.8E-01	BF568633.1	EST_HUMAN	PM1-HT0350-201288-004-b04 HT0350 Homo sapiens cDNA
10807	23141		2.02	4.8E-01	X83502.1	NT	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
11786	24170		1.28	4.8E-01	AL163272.2	NT	S.cerevisiae ORFs from chromosome X
12016	24842		3.04	4.8E-01	AF227565.1	NT	Homo sapiens chromosome 21 segment HS21C027
12646	24895		3.36	4.8E-01	AJ132884.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
8638	19234	32038	8.72	4.7E-01	BF217173.1	EST_HUMAN	Chlamydomonas reinhardtii cap gene, exons 1-8
7107	19447	32263	0.78	4.7E-01	AJ204374.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4098387 5'
7806	20349	33257	0.52	4.7E-01	T11414.1	EST_HUMAN	q772a09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1756544 3'
7808	20349	33258	0.52	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9005	21542	34473	0.6	4.7E-01	8881501	NT	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
10467	22861	35972	0.79	4.7E-01	AW087791.1	EST_HUMAN	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10727	23253		4.94	4.7E-01	AF102873.1	NT	xb88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581580 3'
10963	23478	36503	2.19	4.7E-01	U41069.1	NT	Influenza A virus isolate HK51697 hemagglutinin (HA) gene, partial cds
11163	23670	36715	1.61	4.7E-01	BF528658.1	EST_HUMAN	Human collagen alpha2(XI)(COL11A2) gene, exons 6 through 16, and partial cds
11254	23784	36840	2.89	4.7E-01	AW889448.1	EST_HUMAN	602043889F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5'
11804	24243		1.92	4.7E-01	BE887763.1	EST_HUMAN	RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12036	24325		1.33	4.7E-01	AW341561.1	EST_HUMAN	601811333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3812488 5'
12666	24736		1.38	4.7E-01	AF000007.1	NT	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909188 3'
3797	16397	28862	2.23	4.6E-01	AW818638.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position (7/7)
3806	16406	28870	1.68	4.6E-01	BF683300.1	EST_HUMAN	RC1-ST0278-040400-018-b08 ST0278 Homo sapiens cDNA
3808	16406	28871	1.68	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5323	17885		1.03	4.6E-01	M11267.1	NT	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5429	17886	30390	22.08	4.6E-01	AL163248.2	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C048
5440	17885	30400	1.37	4.6E-01	PS1170	SWISSPROT	AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-SUBUNIT (EPITHELIAL NA+ CHANNEL GAMMA SUBUNIT) (GAMMA ENAC) (NONVOL TAGE-GATED SODIUM CHANNEL 1 GAMMA SUBUNIT) (SCNEG) (GAMMA NACH)
5612	18241	30680	1.12	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
5612	18241	30681	1.12	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
5663	18280	30768	3.27	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18280	30769	3.27	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5735	18361	31067	2.39	4.6E-01	BE734781.1	EST_HUMAN	601568756F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5748	18374	31082	4.22	4.6E-01	A1247678.1	EST_HUMAN	q55h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5748	18374	31083	4.22	4.6E-01	A1247678.1	EST_HUMAN	q55h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5758	18382	31094	1.4	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5828	18452		1.05	4.6E-01	AF212124.1	NT	Andis schwartzii cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5907	18529		0.88	4.6E-01	BE817247.1	EST_HUMAN	PMO-BNC280-120600-001-F07 BN0280 Homo sapiens cDNA
6058	18675	31417	0.75	4.6E-01	D28215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6404	19007	31788	1.05	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165761 to 1176238 (section 100 of 148) of the complete genome
6865	19569	32429	1.36	4.6E-01	U82332.1	NT	Emmericella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6885	19669	32430	1.38	4.6E-01	U82332.1	NT	Emmericella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7712	20221	33108	0.88	4.6E-01	AA493577.1	EST_HUMAN	nt04h05.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8282	20803	33721	13.23	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4287828 5'
9225	21741	34684	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9225	21741	34685	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9583	22083	35046	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9583	22083	35047	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9886	22383	35358	2.63	4.6E-01	A1815634.1	EST_HUMAN	wg73a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
9886	22383	35359	2.63	4.6E-01	A1815634.1	EST_HUMAN	wg73a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10870	23391		3.09	4.6E-01	P88163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10879	23400	36416	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10879	23400	36417	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11346	23044	36054	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11346	23044	36055	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12654	24726		1.26	4.6E-01	M22360.1	NT	Rat plasma proteinase inhibitor alpha-1-inhibitor III group 3 variants 6J, 12J, 13J, and 17J mRNA, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1954	14538	27094	1.89	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1954	14538	27085	1.89	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2895	15512	27982	4.77	4.5E-01	AA877088.1	EST_HUMAN	255d02.61 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3348	15956	28431	0.64	4.5E-01	AW083781.1	EST_HUMAN	xc25c06.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585280 3' similar to gb:L07807
3348	15958	28432	0.64	4.5E-01	AW083781.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
3359	15967	28444	5.18	4.5E-01	Q05783	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3424	18032	28512	1.15	4.5E-01	AF128378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4100	18884		1.35	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4149	18741	29185	0.73	4.5E-01	A1708808.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4255	18015		4.04	4.5E-01	AW873485.1	EST_HUMAN	ss86609.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2353480 3'
5078	17651	30092	1.18	4.5E-01	BE863445.2	EST_HUMAN	h60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5427	17984		26.74	4.5E-01	AF060185.1	NT	601657228R1 NH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5737	18363	31070	1.37	4.5E-01	AW808814.1	EST_HUMAN	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds
6719	18313		1.38	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7449	19867	32834	1.69	4.5E-01	M37036.1	NT	COAT PROTEIN
7804	20117	32893	2.53	4.5E-01	A1858849.1	EST_HUMAN	Rat nuclear proteins B23.1 and B23.2
8249	20780		0.97	4.5E-01	M32881.1	NT	w832a02.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2428818 3' similar to TR:Q82923 Q82923
8342	20883	33904	4.02	4.5E-01	A1848596.1	EST_HUMAN	SWISNF COMPLEX 170 KDA SUBUNIT ;
							D.melanogaster Shaw2 protein mRNA, complete cds
							ts56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282844 3'
8494	21033	33954	0.69	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8716	21256		1.74	4.5E-01	11444769	NT	Homo sapiens hypothetical protein DKFZp47G183 (DKFZp47G183), mRNA
8928	21467	34385	0.69	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
9833	22351		1.02	4.5E-01	9830816	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10389	22883	35877	23.95	4.5E-01	M86008.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cath936206) Homo sapiens cDNA clone HFBCY17
10389	22883	35878	23.95	4.5E-01	M86008.1	EST_HUMAN	EST02531 Fetal brain, Stratiogene (cath936206) Homo sapiens cDNA clone HFBCY17
10744	23288	36285	3.01	4.5E-01	AW591271.1	EST_HUMAN	xc1401.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703885 3' similar to SW:NT8_MOUSE
11131	23639		1.9	4.5E-01	AV719382.1	EST_HUMAN	Q84252 VIRAL INTEGRATION SITE PROTEIN INT-6 [1];
							AV719382 GLC Homo sapiens cDNA clone GLOED12 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11378	23828	36880	1.68	4.5E-01	BE068472.1	EST_HUMAN	RC3-BT0333-160300-018-603 BT0333 Homo sapiens cDNA
11871	26070		3.3	4.5E-01	BE871481.1	EST_HUMAN	601448201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852861 5'
12370	24540		2.13	4.5E-01	BF337631.1	EST_HUMAN	602035275F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183280 5'
12442	24578		6.25	4.5E-01	11422060	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2081	14662		1.39	4.4E-01	0680503	NT	Mus musculus integral membrane-associated protein 1 (limap1), mRNA
2432	14899	27572	3.26	4.4E-01	P40785	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (MEGF RELATED FACTOR)
3357	15985	28442	1.27	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3357	15985	28443	1.27	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3361	15969	28446	2.31	4.4E-01	BF066726.1	EST_HUMAN	7891492.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3383785 5'
4318	16804		1.28	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608393 5'
5134	17706		2.07	4.4E-01	BE141398.1	EST_HUMAN	MR0-HT0078-131288-007-g05 HT0078 Homo sapiens cDNA
5277	17839	30285	0.94	4.4E-01	U81154.1	NT	Buzura suppressaria nucleopolydnavirus ecdyseroid UDP-glucosyltransferase (egt) gene, complete cds
5417	17874		0.8	4.4E-01	AW814885.1	EST_HUMAN	MR1-ST0206-120400-022-g07 ST0206 Homo sapiens cDNA
5613	18242	30892	4.06	4.4E-01	PO4829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5613	18242	30893	4.06	4.4E-01	PO4829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5887	18489	31215	1.72	4.4E-01	S65019.1	NT	much [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5883	18505	31231	1.9	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
6108	18724	31476	1.53	4.4E-01	A189413.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR-Q29168 Q29168 UNKNOWN PROTEIN
6108	18724	31477	1.53	4.4E-01	A189413.1	EST_HUMAN	q62h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR-Q29168 Q29168 UNKNOWN PROTEIN
6387	18990	31771	1.69	4.4E-01	AW080785.1	EST_HUMAN	xc-27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR-O85154 O85154 AFLATOXIN B1-ALDEHYDE REDUCTASE
6470	19071		1.02	4.4E-01	AA776132.1	EST_HUMAN	ae65d11.s1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:970865 3' similar to gb.M16038
7429	19953	32818	0.99	4.4E-01	AE000571.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN); Helicobacter pylori 26695 section 49 of 134 of the complete genome
7782	20325		10.05	4.4E-01	Z11679.1	NT	S. luteus mRNA for induced stolon tip protein (partial)
8688	21237	34160	1.01	4.4E-01	AA058427.1	EST_HUMAN	z68a03.s1 Stratiotes schizobrain (#637204) Homo sapiens cDNA clone IMAGE:508836 3'
9078	21814	34549	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9111	21847	34587	0.56	4.4E-01	AW612578.1	EST_HUMAN	h105c08.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6
9214	21731	34874	1.13	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9872	22369	35347	1.69	4.4E-01	A1268650.1	EST_HUMAN	q03909.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910821 3'
9873	22370		2.12	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10009	22504	35495	4.51	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10276	22771	35759	1.43	4.4E-01	S76404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8963 nt, segment 2 of 2]
10276	22771	35760	1.43	4.4E-01	S76404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8963 nt, segment 2 of 2]
11939	24271	31018	4.68	4.4E-01	6877874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
11952	25000		14.98	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12517	24635		1.5	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
436	13069	25564	1.77	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
436	13069	25565	1.77	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
3096	15711	28182	0.91	4.3E-01	AW699477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4231	16819	29268	1.21	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4495	13069	25564	3.96	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
4495	13069	25565	3.96	4.3E-01	AF155218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
5567	18188	30645	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5567	18188	30646	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6049	18668	31407	1.34	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0639-070500-181-408 HT0638 Homo sapiens cDNA
6065	18682	31424	2.06	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC186) gene, partial cds
6809	19400	32215	4.28	4.3E-01	AJ001678.1	NT	Columba coturnix japonica ifnG gene
6949	19528		0.78	4.3E-01	Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
7456	19680		1.78	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158298 5'
8366	20906		2.66	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-flaI) genes, complete cds
9179	21758	34702	0.7	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9642	22142	35109	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
9642	22142	35110	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
10126	22623	35614	0.57	4.3E-01	AW170558.1	EST_HUMAN	xt63a05.x1 Soares_NHCoC_cervical_tumor Homo sapiens cDNA clone IMAGE:2868400 3' similar to
10811	19016	32451	2.52	4.3E-01	AF075629.1	NT	TR:000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ;
11588	24031	37101	1.54	4.3E-01	A1874332.1	EST_HUMAN	Equus caballus microsatellite LEX027
11632	18198	30645	1.55	4.3E-01	P48634	SWISSPROT	t284404.x1 NCL_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2283351 3'
11632	18198	30646	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
12616	24696		2.81	4.3E-01	AJ003022.1	NT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
1402	15440	26524	1.39	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor whiH gene
1891	14573		1.04	4.2E-01	AA761653.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
							n224a09.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288696 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2068	14646		1.37	4.2E-01	AF258325.1	NT	Plasmodium falciparum multidrug resistance protein Pgh1 gene, complete cds
3689	16270	28738	4.91	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3689	16300	28768	1	4.2E-01	AI280338.1	EST_HUMAN	q194b01.x1 Soares_NHt-MP_u_S1 Homo sapiens cDNA clone IMAGE:1878945 3'
3773	18014		0.6	4.2E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40488
3948	18546	28014	0.73	4.2E-01	AW83527.1	EST_HUMAN	QV0-L T0015-180200-127-h01 LT0015 Homo sapiens cDNA
4054	18851	29118	0.98	4.2E-01	Q04888	SWISSPROT	SOX-8 PROTEIN
4807	17395	28835	4.3	4.2E-01	AA594088.1	EST_HUMAN	np68h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb.M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4895	17470	28928	4.04	4.2E-01	R13467.1	EST_HUMAN	Y77601.r1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:28278 5'
5232	17708		3.77	4.2E-01	U08071.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
5881	18514	31241	1.52	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108483 5'
5953	18575	31308	2.16	4.2E-01	AW854182.1	EST_HUMAN	RC3-CT0254-080400-029-g04 CT0254 Homo sapiens cDNA
6952	18957	31736	1.06	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7031	19565	32382	10.28	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7031	19565	32383	10.28	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7082	24776	32492	1.97	4.2E-01	S82504.1	NT	Brcal1=breast cancer gene [rats, W.F. spleen, Genomic, 419 nt, segment 2 of 2]
7150	19883	32524	5.81	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7834	20476	33385	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGe resequences, MAGe Homo sapiens cDNA
7834	20476	33388	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGe resequences, MAGe Homo sapiens cDNA
8148	20689	33602	0.55	4.2E-01	4756039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
8235	21761	34708	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
8235	21761	34707	0.52	4.2E-01	U67431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
8980	22377		0.81	4.2E-01	AA705007.1	EST_HUMAN	z89f01.s1 Soares_fetal_liver_INFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10083	22578	35571	0.5	4.2E-01	AF181854.1	NT	Lassa virus strain 803273 glycoprotein precursor and nucleoprotein genes, complete cds
10390	22884	35879	1.35	4.2E-01	AW865668.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
10821	23440	38461	3.68	4.2E-01	AB023488.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11273	23726	36780	2.65	4.2E-01	BE968485.2	EST_HUMAN	801680352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806085 3'
12561	24661		1.49	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5'
1133	13736	26245	1.59	4.1E-01	AI805481.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1142	13745	26254	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1142	13745	26255	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2735	15280	27858	1.58	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2807	15582	28061	2.11	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2967	15682	28062	2.11	4.1E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3342	15652	28428	0.68	4.1E-01	AA906344.1	EST_HUMAN	q94b08.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3839	18438	28899	0.58	4.1E-01	AW961202.1	EST_HUMAN	EST1373364 IMAGE resequences, MAGG Homo sapiens cDNA
3839	18438	28900	0.58	4.1E-01	AW961292.1	EST_HUMAN	EST1373364 IMAGE resequences, MAGG Homo sapiens cDNA
4361	18948	29390	2.82	4.1E-01	AJ248207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4363	16978		0.76	4.1E-01	AA908257.1	EST_HUMAN	om33d02.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4774	17355	29607	1.31	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPC8DF10 5'
6141	18755	31513	3.97	4.1E-01	BF681383.1	EST_HUMAN	602156580F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4297319 5'
7460	18983	32848	2.74	4.1E-01	U87535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7979	20521	33427	1.31	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288238 5'
9019	21556	34484	1.26	4.1E-01	6755521	NT	Mus musculus signalling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
9484	21941		0.61	4.1E-01	AF160597.1	NT	Volvox gymnocaudus Vgym580 cytochrome b (cytb) gene, complete cds, mitochondrial gene for
10184	22859		1.26	4.1E-01	AL138076.2	NT	mitochondrial product
10310	22804	35798	0.79	4.1E-01	AV649578.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome, segment 3/6
10401	22895	35800	0.51	4.1E-01	P18584	SWISSPROT	AV649578 GLC Homo sapiens cDNA clone GLC8VD12 3'
10401	22895	35891	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10471	22865		2.28	4.1E-01	BF349382.1	EST_HUMAN	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10719	23247	36282	45.22	4.1E-01	X68700.1	NT	CM2-HT0137-200989-010-408 HT0137 Homo sapiens cDNA
11270	23008	36015	3.57	4.1E-01	Q08470	SWISSPROT	Zea mays ZmPMS2 gene for 19 kDa zinc protein
12280	25049		2.6	4.1E-01	D67675.1	NT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
147	15408		4.55	4.0E-01	AW847123.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
1077	13681	28191	0.82	4.0E-01	B404858	NT	RC2-CT0201-200989-012-410 CT0201 Homo sapiens cDNA
1384	13978	28505	1.51	4.0E-01	AF203478.1	NT	Laqueus rubellus mitochondrion, complete genome
1532	14124		4.1	4.0E-01	6879258	NT	Drosophila melanogaster Dalmation (dnt) mRNA, complete cds
2049	15458	27200	1.22	4.0E-01	Z98833.1	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2049	15458	27201	1.22	4.0E-01	Z98833.1	NT	Aesobolus limersus mesc2 gene
2204	14780	27352	17.82	4.0E-01	AE001931.1	NT	Aesobolus limersus mesc2 gene
2204	14780	27353	17.82	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2631	12811	25289	1.45	4.0E-01	6878490	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2695	15511	28090	1.23	4.0E-01	AL163280.2	NT	Mus musculus ubiquitin-protein ligase e3 component n-recognition (Ubr1), mRNA
2695	15511	28091	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2695	15511	28091	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	16359	28828	2.17	4.0E-01	AF088903.1	NT	Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3889	16408	28900	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3889	16408	28901	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4942	17517		8.41	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6069	18898	31428	1.16	4.0E-01	AW970610.1	EST_HUMAN	EST382691 IMAGE resequencing, MAGK Homo sapiens cDNA
6567	19165	31981	0.87	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P139) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7777	20286	33183	0.72	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7869	20411	33317	0.46	4.0E-01	BF082634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7954	20490	33408	0.89	4.0E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
8836	21474	34394	0.98	4.0E-01	AA323289.1	EST_HUMAN	EST28068 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11443	23893		1.95	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
11568	24015		3.52	4.0E-01	L76800.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
11658	24801		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12518	24836		1.42	4.0E-01	P38049	SWISSPROT	HYPOTHEICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1420	14013	26543	1.98	3.8E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2668	15226	27798	3.8	3.8E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2730	15265	27851	3.79	3.8E-01	X82032.1	NT	H.sapiens B-myb gene
2730	15286	27852	3.79	3.8E-01	X82032.1	NT	H.sapiens B-myb gene
3131	15745	28214	3.95	3.8E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syrB2, cys3 genes and orf3
4153	16745	29199	1.49	3.8E-01	BF582811.1	EST_HUMAN	7161401.x1 NC1_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5130	17702	30136	1.86	3.8E-01	BE728687.1	EST_HUMAN	601563949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833689 5'
6090	18706	31454	6.44	3.8E-01	BF208038.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
8428	18028	31812	0.68	3.8E-01	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xg28STS protein (XG28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7898	20438	33343	0.78	3.8E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
8795	21334	34259	0.73	3.8E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170898-004-b08 CT0105 Homo sapiens cDNA
8804	21343		0.7	3.8E-01	BF348634.1	EST_HUMAN	602018944F1 NC1_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158322 5'
9161	21696	34840	1.24	3.8E-01	AW195888.1	EST_HUMAN	m86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821
							OB4821 KIAA0713 PROTEIN ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9484	21889	34845	1.42	3.8E-01	A693737.1	EST_HUMAN	wp76a02.x1 NCL_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
9792	22280	35274	3.68	3.8E-01	M19879.1	NT	SW_RFX5_HUMAN P48382 BINDING REGULATORY FACTOR. ;
9858	22354		0.5	3.8E-01	11485620	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10071	22568	35581	0.69	3.8E-01	D88722.1	NT	Porphyra purpurea mitochondrion, complete genome
10482	22886	35983	0.46	3.8E-01	M18440.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10700	23229		1.82	3.8E-01	AV695974.1	EST_HUMAN	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
11729	24977		3.42	3.8E-01	AF304354.1	NT	AV695974 GKC Homo sapiens cDNA clone GKCBQC11 5'
11854	24214		1.42	3.8E-01	Q61670	SWISSPROT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
11890	24285	31015	1.58	3.8E-01	AE001811.1	NT	HOMEOBOX PROTEIN HLX1
12389	24551		1.37	3.8E-01	11433335	NT	Thermotoga maritima section 123 of 136 of the complete genome
171	12834		19.28	3.8E-01	7019488	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
531	13182		3.11	3.8E-01	AB029281.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1811	14488		0.89	3.8E-01	AE003870.1	NT	Mus musculus pem-1 mRNA for pericentriolar material-1, complete cds
2805	15167	27734	1.89	3.8E-01	AF214117.1	NT	Xylella fastidiosa, section 18 of 229 of the complete genome
2861	15473	27781	3.94	3.8E-01	6878002	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
3034	15650		0.89	3.8E-01	AJ251057.1	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3084	15689	28173	2.2	3.8E-01	AF043383.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP-1213)
3530	16135	28815	9.83	3.8E-01	AL161518.2	NT	Pleurococcus americanus aminopeptidase N (ampN) gene, partial cds
3592	16168		0.59	3.8E-01	AB07219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3609	16189		0.75	3.8E-01	AB07219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3820	16420	28882	0.94	3.8E-01	BE154080.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3989	16587	29058	0.8	3.8E-01	6754096	NT	PMO-H10339-200400-010-G01 HTD339 Homo sapiens cDNA
4138	16730	29183	0.69	3.8E-01	AJ271361.2	NT	Mus musculus general transcription factor II I (Gtf2i), mRNA
5271	17833	30259	0.99	3.8E-01	BE544953.1	EST_HUMAN	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
							601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
							yf8a11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210428 5' similar to
							gb M87833 HUMALU384 Human carcinoma cell-derived Alu RNA transcript (rRNA); gb M86858
							EPIDERMAL GROWTH FACTOR-LIKE CRYPTO PROTEIN (HUMAN); contains Alu repetitive
							element; contains MER4 repetitive element ;
5412	17989	30378	1.07	3.8E-01	H84627.1	EST_HUMAN	TRANSCRIPTION FACTOR SOX-10
5794	18419	31135	1.11	3.8E-01	Q04888	SWISSPROT	p10n protein [mink, Genomic, 2446 nt]
6481	19082		0.68	3.8E-01	S48825.1	NT	
6737	19331	32137	5.29	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-402 BT0537 Homo sapiens cDNA
							la54f11.x1 Soares total fetus_Nb2IFB_gw Homo sapiens cDNA clone IMAGE:2047817 3' similar to
6857	19391	32423	3.97	3.8E-01	A1374601.1	EST_HUMAN	contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7019	19517	32339	1.33	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7626	20045		4.75	3.8E-01	X61597.1	NT	M. musculus gene for kallikrein-binding protein
8238	20778	33700	0.49	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8402	21031	33951	2.34	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8560	21089	34019	1.14	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8751	21280	34210	1.12	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9480	21879		4.03	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element
11408	23859		3.5	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11541	23989	37080	2.95	3.8E-01	R42550.1	EST_HUMAN	Y62h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11541	23989	37061	2.95	3.8E-01	R42550.1	EST_HUMAN	Y62h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11940	24272		2.81	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12068	24688		1.75	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12189	24421		1.45	3.8E-01	BE829258.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
12565	24884		2.22	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
12838	24713	30886	1.25	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2521	15085	27657	15.01	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3507	16112	28589	10.94	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3838	16538	29003	0.88	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4313	16889	29344	9.19	3.7E-01	AI218707.1	EST_HUMAN	ck9ec07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510186 3'
4412	16997	29440	1.18	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4479	17064	29514	3.13	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5838	18557	31285	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6105	18721	31474	0.94	3.7E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
6633	18229	32033	1	3.7E-01	M10808.1	NT	Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds
6651	18247		0.81	3.7E-01	L10353.1	NT	Mus saxicola heptoglobin mRNA, complete cds
7197	19728	32579	4.44	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
8271	20812	33733	1.88	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8271	20812	33734	1.88	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8306	20847	33770	0.76	3.7E-01	AA902812.1	EST_HUMAN	ck43b11.s1 NC1_CGAP_La2 Homo sapiens cDNA clone IMAGE:1516701 3'
9129	21664		1.54	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10074	22569		0.46	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exon region
10111	22808	35568	4.17	3.7E-01	AF368411.1	EST_HUMAN	qt46b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950987 3'
10809	23428	36446	3.47	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10909	23428	38447	3.47	3.7E-01	AJ287357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11341	23039	36048	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11549	23907		1.8	3.7E-01	AA973540.1	EST_HUMAN	ccf6d03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698
11603	24046		2.76	3.7E-01	6877878	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
11640	24601		1.82	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11821	24191		4.15	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
11913	24251		4.72	3.7E-01	D86878.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12302	24489		2.94	3.7E-01	AL121154.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12377	24545	30804	7.01	3.7E-01	Y18000.1	NT	DKFZp762K075_r1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
282	12638	25424	1.07	3.6E-01	AJ009609.1	NT	Homo sapiens NF2 gene
1033	13643		8.45	3.6E-01	U89241.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1357	13951	28477	4.32	3.6E-01	T80255.1	EST_HUMAN	Human mibp gene, partial cds
1959	14543	27089	6.39	3.6E-01	T80255.1	EST_HUMAN	y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1959	14543	27100	6.39	3.6E-01	AW590184.1	EST_HUMAN	y03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1994	14576	27138	7.23	3.6E-01	AF216207.1	NT	hg33102.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
2088	14877		0.88	3.6E-01	AF056927.1	NT	hg33102.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
2309	14881		1.13	3.6E-01	AB002321.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2433	15000		2.49	3.6E-01	X76725.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2528	15082	27665	3.34	3.6E-01	AW812033.1	EST_HUMAN	Human mRNA for KIAA0323 gene, partial cds
							P. irregularis (P3804) gene for actin
							RC5-STD171-191099-011-g07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2859	15218	27789	1.38	3.6E-01	P24206	SWISSPROT	
2824	18012		10.38	3.6E-01	AF169485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3516	16121	28600	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3516	16121	28601	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4497	17081	28530	1.97	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
4850	17428	28680	0.94	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4867	17443	28684	0.65	3.6E-01	Y11528.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5153	17723	30154	2.28	3.6E-01	AW336389.1	EST_HUMAN	hs02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568 3'
5261	17824	30249	0.58	3.6E-01	BE067689.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
6236	18845	31616	1.16	3.6E-01	P10431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6804	18201	32006	1.68	3.0E-01	Y10196.1	NT	Homo sapiens PH1EX gene
7202	19733		4.57	3.0E-01	R04090.1	EST_HUMAN	Y74406.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:275987 5'
7327	19854	32717	1.73	3.0E-01	AW027174.1	EST_HUMAN	w472c10.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8168	20707	33623	0.68	3.0E-01	P98167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1];
8221	20762	33676	13.59	3.0E-01	AL161583.2	NT	SC0-SFONDIN
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8832	21470	34388	3.06	3.0E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8832	21470	34388	3.06	3.0E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9120	21658	34597	1.32	3.0E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9320	21834	34784	0.92	3.0E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9320	21834	34785	0.92	3.0E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9390	21813		0.54	3.0E-01	X62825.1	NT	C. parvifrons plc gene for phospholipase C upstream region containing bent DNA fragment
9777	22275	35260	18.15	3.0E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9804	22401	35374	0.53	3.0E-01	AW752801.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9904	22401	35376	0.53	3.0E-01	AW752801.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10823	23344	36359	2.51	3.0E-01	BE902390.1	EST_HUMAN	601678418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958897 5'
10937	23501	36531	4.15	3.0E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11065	23577	36815	2.02	3.0E-01	L41687.1	NT	Mus musculus T-cell receptor V region delta 1 chain gene, 5' region
							Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11318	23016	36025	4.07	3.0E-01	AE000856.1	NT	Homo sapiens h1b5 gene for hair keratin, exons 1 to 9
11680	25109		2.45	3.0E-01	Y19210.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
11768	24159		5.79	3.0E-01	AE000335.1	NT	Mus musculus Enr1 mRNA, complete cds
11823	24258		4.7	3.0E-01	U66888.1	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (vithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12308	24502		2.16	3.0E-01	11432568	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
120	12781	25273	1.35	3.0E-01	AL161536.2	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
223	12884	25369	2.67	3.0E-01	6678933	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
706	13327	25814	4.48	3.0E-01	AL161581.2	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
754	13373	25868	1.39	3.0E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
754	13373	25868	1.39	3.0E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
812	13430	25935	3.83	3.0E-01	BF128796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1682	14274	26807	1.91	3.5E-01	U35778.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2322	14893	27469	1.12	3.5E-01	P06708	SWISSPROT	HOMEOBOX PROTEIN HOXA-4 (HOX-1.4) (MH-3)
2637	15472	27770	1.92	3.5E-01	AA223262.1	EST_HUMAN	z08a09.e1 Striatogene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2729	15284		11.8	3.5E-01	U05897.1	NT	Fibroblast succinoglycogen S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
3030	15946	28124	0.57	3.5E-01	AA057891.1	EST_HUMAN	z04f03.r1 Striatogene corneal stroma (#837222) Homo sapiens cDNA clone IMAGE:512285 5'
3878	16476		1.27	3.5E-01	AA842138.1	EST_HUMAN	m00403.s1 NCL CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4349	16936	29377	2.3	3.5E-01	AF071293.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds
5014	17588	30031	0.57	3.5E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07878, Z40498
5066	17639	30082	4.33	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
5537	18169	30583	0.74	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5537	18169	30584	0.74	3.5E-01	Q86887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5738	18364	31071	1.42	3.5E-01	D42045.1	NT	Human mRNA for KIAA0098 gene, complete cds
6384	18988		0.9	3.5E-01	AW863816.1	EST_HUMAN	PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA
6540	19139	31932	0.75	3.5E-01	AA431833.1	EST_HUMAN	z07903.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782428 5' similar to TR: 1066935
6578	19176	31976	0.72	3.5E-01	U37150.1	NT	G1068935 F10F2.1;
6770	19363	32172	0.93	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7116	19458		3.51	3.5E-01	X86605.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
8016	20558		2.02	3.5E-01	1148042	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
8019	20561	33482	0.65	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8403	20943		0.61	3.5E-01	AF061691.1	NT	RC4-ET0024-280600-014-007 ET0024 Homo sapiens cDNA
8857	21396	34319	1.12	3.5E-01	4507810	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9651	22150	35120	1.83	3.5E-01	Q02284	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9801	22288	35284	4.91	3.5E-01	Z8825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9877	22374	35351	1.14	3.5E-01	BE174794.1	EST_HUMAN	X.lavis gene for albumin including HP1 enhancer
10613	23146	36157	4	3.5E-01	X61084.1	NT	QV2-HT0577-080400-128-c07 HT0577 Homo sapiens cDNA
10802	23422	36440	2.08	3.5E-01	AJ243178.1	NT	C.griseus rhodopsin gene for opsin protein
10802	23422	36441	2.08	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11482	23912	36979	1.93	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11532	23980	37050	1.71	3.5E-01	L05145.1	NT	y08012.r1 Soares_multiple_sclerosis_2NbrMSP Homo sapiens cDNA clone IMAGE:280375 5'
							Human glucokinase (GCK) gene, repeat polymorphism

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11778	25112		1.51	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
11851	24211		7.56	3.5E-01	X64955.1	NT	B. taurus atpA1 gene for F(0F(1) ATP synthase alpha-subunit
12014	24313		2.03	3.5E-01	AE001774.1	NT	Thermotoga maritima section 88 of 138 of the complete genome
12209	24433		2.21	3.5E-01	AE001691.1	NT	Thermotoga maritima section 3 of 138 of the complete genome
12643	24950	30625	2.84	3.5E-01	H80814.1	EST_HUMAN	ys84f11.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
12843	24950	30628	2.84	3.5E-01	H80814.1	EST_HUMAN	ys84f11.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
736	13356		1.5	3.4E-01	AJ242858.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1011	13621	26136	7.62	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens cdlR, cdlS genes, orf222 and partial inaA gene
1013	13623	26138	8.97	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0281-241189-019-g10 HT0281 Homo sapiens cDNA
1371	13965	28491	1.86	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2445	15012	27594	2.6	3.4E-01	D80809.1	NT	Synechocystis sp. PCC6803 complete genome, 1127, 1311235-1430418
3032	15648	28126	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3032	15648	28127	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3163	15798	28268	0.66	3.4E-01	D80809.1	NT	Synechocystis sp. PCC6803 complete genome, 1127, 1311235-1430418
3197	15809	28282	6.78	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3387	15896	28473	0.84	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3594	16188	28671	4.84	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3858	16456		1.32	3.4E-01	BF449010.1	EST_HUMAN	7f84a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8LUJ15
4108	16702		1.23	3.4E-01	AF184614.1	NT	Q8LUJ15 DJ18C9.1 ;
4126	16718		1.56	3.4E-01	AA584196.1	EST_HUMAN	Homo sapiens p47-phox (NCF1) gene, complete cds
4594	17177	28624	0.7	3.4E-01	AF166341.1	NT	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4749	17330	28773	2	3.4E-01	BE068912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4765	17348	28795	1.01	3.4E-01	BF314688.1	EST_HUMAN	MIR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5087	17660		4.2	3.4E-01	A1240973.1	EST_HUMAN	601901632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130335 5'
5864	18486	31210	2.9	3.4E-01	AL161594.2	NT	q85c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1667208 3' similar to contains Alu repetitive element
5979	18569		5.68	3.4E-01	AA065313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
6158	18771		2.44	3.4E-01	L02871.1	NT	zn12d11.s1 Streptococcus hnt neuron (8637233) Homo sapiens cDNA clone IMAGE:547221 3'
							Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6181	18791	31560	0.69	3.4E-01	BE748912.1	EST_HUMAN	60157181T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3839826 3'
6258	18865	31635	2.45	3.4E-01	AW204505.1	EST_HUMAN	UI-H-B11-est-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718582 3'
6382	18886	31768	1.02	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6841	19431		1.32	3.4E-01	N86225.1	EST_HUMAN	zb53e12.s1 Soares_fetal_lung_NihHL19W Homo sapiens cDNA clone IMAGE:307342 3'
							hm63g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
7027	19561	32388	1.09	3.4E-01	AI468082.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7847	20369		0.51	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8179	20720	33635	0.51	3.4E-01	Y14930.1	NT	Homo sapiens TCRV28 gene, allele A4, partial
8424	20804		1.92	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
8498	21037	33958	0.88	3.4E-01	L04690.1	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
8788	21325	34249	1.63	3.4E-01	8633624	NT	Bovine enterovirus strain K2577, complete genome
9139	21674	34616	3.89	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9139	21674	34617	3.89	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9342	21856		0.59	3.4E-01	AB017610.1	NT	Epithelial fibroblast mRNA for PLC-gammaS, complete cds
9367	20306	33208	4.77	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9367	20306	33208	4.77	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9612	22112	35075	0.86	3.4E-01	U88763.1	NT	Glycine max putative transcription factor SCOF-1 (scsf-1) mRNA, complete cds
9804	22302	35288	1.99	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10373	22867		0.54	3.4E-01	AE004098.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
							Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome
10885	23416		4.42	3.4E-01	AE000881.1	NT	PROBABLE E4 PROTEIN.
10932	23450	36471	2.61	3.4E-01	P08923	SWISSPROT	
10989	23484	36512	2.72	3.4E-01	AF045981.1	NT	Rudius erasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11164	23671	36716	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11164	23671	36717	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11372	23824	36887	2.27	3.4E-01	AB035607.1	NT	Rattus norvegicus mRNA for s-glycerol/ALC18, complete cds
11401	23852	36917	4.36	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11614	24056	37121	1.75	3.4E-01	BF081948.1	EST_HUMAN	7688d12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3480846 3'
11655	24082		2.12	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
11771	24180		1.44	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
11873	24836		1.8	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwif8p (cwif8) gene, complete cds
11998	24303		14.59	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12023	24865		3.18	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12078	24974		2.44	3.4E-01	9838361	NT	PTR5 repetitive element;
12198	24424	30950	2.68	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
12427	25068		1.25	3.4E-01	AJ288948.1	NT	Mus musculus SIL_MAP_17, CYP_a, SCL & CYP_b genes
							Clostridium cellulosum partial spoVB gene and spoDA gene, strain ATCC 35319
12623	24639		2.55	3.4E-01	AF010413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes;>
12651	24723		2.71	3.4E-01	11406174	NT	Neisseria glabrata mitochondrion, complete genome
16	12685	25151	13.68	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
110	12686	25151	3.75	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
473	13108	25589	1.08	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
661	13285	25768	1.87	3.3E-01	7682485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1242	13940	28358	2.06	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1350	13945	28468	3.58	3.3E-01	BF588880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4900251 3'
1649	14241	28775	1.43	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1773	14363		1.44	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week I Homo sapiens cDNA 5' end
2075	14655		1.22	3.3E-01	AF031148.1	NT	Methylobacterium capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2450	15017		5.41	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (urate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMP5) mRNA
2976	15592	28074	2.14	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
3049	15665		0.68	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3061	15708	28178	0.82	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus nitramycin biosynthetic genes
3542	16147	28628	0.99	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3882	16480	28942	2.14	3.3E-01	O94645	SWISSPROT	EXOEOXYRIBONUCLEASE V BETA CHAIN
3890	16489	28949	0.85	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4037	16635	29104	1.49	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4073	16669	29130	1.95	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4457	17043		1.44	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4789	17377		1.57	3.3E-01	A1639114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb.X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4964	17538	28980	1.44	3.3E-01	D94003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18159	30573	2.75	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5527	18159	30574	2.75	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
6101	18171	31468	1.72	3.3E-01	BE819650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6101	18171	31469	1.72	3.3E-01	BE819650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6168	18798	31567	12.71	3.3E-01	P05691	SWISSPROT	CIRCULIMSPOROZOITE PROTEIN (CS)
6869	19546	32369	4.8	3.3E-01	A1628131.1	EST_HUMAN	tye4h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6869	19546	32370	4.8	3.3E-01	A1628131.1	EST_HUMAN	tye4h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7758	20268	33182	1.61	3.3E-01	N85148.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8497	21038	33957	17.55	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8663	21202	34120	0.48	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
8696	21235	34157	0.49	3.3E-01	AU128115.1	EST_HUMAN	AU128115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8696	21235	34158	0.49	3.3E-01	AU128115.1	EST_HUMAN	AU128115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9042	21578	34508	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9300	21900	34848	0.99	3.3E-01	BE828481.1	EST_HUMAN	GM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9300	21900	34849	0.99	3.3E-01	BE828481.1	EST_HUMAN	GM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9430	21939	34887	3.24	3.3E-01	N69868.1	EST_HUMAN	z687h01.s1 Soares_fetal_kung_NihHL19W Homo sapiens cDNA clone IMAGE:297849 3'
9471	21970	34819	2.93	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9902	22389		2.16	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10600	23134	36147	2.83	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10600	23134	36148	2.83	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10805	23424		1.8	3.3E-01	BF528488.1	EST_HUMAN	602070802F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213585 5'
11110	23620	36861	17.52	3.3E-01	BE219651.1	EST_HUMAN	hy51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
11223	23754	36812	4.97	3.3E-01	P47953	SWISSPROT	cb71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11565	24012		4.68	3.3E-01	AA808621.1	EST_HUMAN	RH2abium leguminosarum sym plasmid pRL5LJ nodX gene
11584	12685	25151	2.48	3.3E-01	X07890.1	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
11759	24153	36771	1.96	3.3E-01	6598319	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
12510	24631		36.28	3.3E-01	AP000002.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
482	13115		1.79	3.2E-01	AF018261.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13387		0.76	3.2E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1204	13804	26317	27.96	3.2E-01	AF047013.1	NT	Fusarium rose virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1325	13818	26441	1.39	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1434	14027	26555	7.37	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1811	14401	26946	0.92	3.2E-01	Z38041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1819	14408	26954	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1819	14409	26955	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1883	14468	27028	1.22	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2205	14781	27354	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2578	15140		2.24	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxct1), mRNA
2734	15288	27857	1.09	3.2E-01	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3068	16268		0.78	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4023	16821		0.61	3.2E-01	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4483	17088	28518	1.64	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4597	17181	28628	1.58	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4844	17422		6.52	3.2E-01	BF683817.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5009	17582	30025	0.63	3.2E-01	Q57061	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P99)
5174	17741	30170	0.58	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868799 5'
5392	17850	30363	0.93	3.2E-01	AY008947.1	NT	Homo sapiens Interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5478	18110	30519	2.5	3.2E-01	BE173884.1	EST_HUMAN	CMD-HT05689-080300-289-f10 HT05689 Homo sapiens cDNA
6112	18728	31481	1.18	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6831	19421		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8113	20654	33563	1.33	3.2E-01	M80286.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8210	20751	33665	0.51	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12Wax1
8308	20849	33772	11.34	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8311	20852	33777	16.78	3.2E-01	BF311635.1	EST_HUMAN	601867107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8388	20898		1.43	3.2E-01	AL181674.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8437	20977	33891	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8437	20977	33892	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8508	21047	33868	2.72	3.2E-01	AE02015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8605	21144	34058	0.69	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8805	21144	34059	0.89	3.2E-01	U51028.1	NT	Oryzobolus curticulus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8897	21535	34465	0.58	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9007	21544		2.08	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9077	21613	34547	0.48	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9077	21613	34548	0.48	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9805	22402	35378	3.22	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
10100	22585	35588	0.51	3.2E-01	BE326230.1	EST_HUMAN	h89805.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181568 3'
10213	22708		3.03	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10548	23084	36088	3.28	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFB0221
11786	24989		4.31	3.2E-01	L07288.1	NT	Drosophila melanogaster leminin A (Lam-A) mRNA, complete cds
12344	24525		4.85	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12441	24819		3.37	3.2E-01	AF157625.1	NT	Bos taurus insulin 1,4,5-trisphosphate receptor type I mRNA, complete cds
12488	24818		1.94	3.2E-01	L39874.1	NT	Homo sapiens deoxydicydylate deaminase gene, complete cds
12560	25041	30504	1.98	3.2E-01	BE385778.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818748 5'
2685	15252	27823	2.39	3.1E-01	R18051.1	EST_HUMAN	ye601h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M84241 QM PROTEIN (HUMAN);
2722	15403	27843	3.67	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2722	15403	27844	3.67	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2883	15501		1.35	3.1E-01	AW628038.1	EST_HUMAN	h46h08.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3208	15820		3.53	3.1E-01	AB028068.1	NT	Mus musculus gene for Ser/Thr kinase KIAA0174, exon 8
3978	16578	29046	0.91	3.1E-01	AJ251598.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5055	17628	30072	0.78	3.1E-01	S88245.1	NT	carbonic anhydrase IV [rats, Sprague-Dawley, lung, mRNA, 1205 nt]
5097	17670	30109	0.82	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5208	17771	30194	0.98	3.1E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5688	18298	30776	10.8	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5786	18411	31127	0.75	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141w
5786	18421		0.99	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polyoystin
5945	18565	31285	2.16	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6582	19189	31982	2.63	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6854	18250	32052	0.87	3.1E-01	AJ284458.1	EST_HUMAN	q139d01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874689 3'
6784	19375	32181	0.81	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6883	19597		0.9	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-261089-005-h05 CT0222 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	24741	30458	2.4	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5'
7671	20183	33071	1.18	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8582	21121	34041	1.22	3.1E-01	R45318.1	EST_HUMAN	YG46101.s1 Soares infant brain T11B Homo sapiens cDNA clone IMAGE:35639 3'
9816	22314	35295	0.45	3.1E-01	6876322	NT	Mus musculus phosphatidylinositol 4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
9879	22474	35456	0.81	3.1E-01	BF686839.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
9879	22474	35457	0.81	3.1E-01	BF686839.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10035	22530	35525	1.7	3.1E-01	A1244001.1	EST_HUMAN	q61e11.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S65700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10204	22699		0.54	3.1E-01	T55325.1	EST_HUMAN	y647h08.s1 Stratigene fetal spleen (8637205) Homo sapiens cDNA clone IMAGE:74967 3' similar to similar to gb:1M91036_maz2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10717	23245	36261	1.95	3.1E-01	BF216117.1	EST_HUMAN	601983592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11411	23862	36823	2.03	3.1E-01	7662281	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11821	24257		2.13	3.1E-01	AF294308.1	NT	Andis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
11980	24282		1.95	3.1E-01	AF304182.1	NT	Sitosterolemia vitreum 40S ribosomal protein S11 mRNA, partial cds
12108	24370		3.31	3.1E-01	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12496	24624		3.89	3.1E-01	AF108779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, complete cds; and L-type calcium channel α
12535	25035		1.62	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp-pending), mRNA
76	15382	25234	1.37	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Ptkce), mRNA
275	12932	25419	11.51	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1268	13883	26380	2.05	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2774343 3'
1555	14147	26680	6.64	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
3248	15860		1.4	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3932	16530	26897	2.1	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261189-001-g01 ST0262 Homo sapiens cDNA
4046	16643	29109	1.01	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4611	17184	29640	1.78	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5554	18186	30601	5.34	3.0E-01	BE741629.1	EST_HUMAN	601584900F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5627	18256	30726	0.88	3.0E-01	AF228247.1	NT	Caragato orthopoxvirus hemagglutinin gene, complete cds
5685	18321	30820	4.03	3.0E-01	BE688575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5685	18321	30821	4.03	3.0E-01	BE688575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5731	18357	31062	4.57	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6819	19578	32407	3.14	3.0E-01	D16131.1	NT	Mouse cytokeratin 15 gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6844	18052	30476	0.7	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/87 kDa laminin-binding protein mRNA, partial cds
7005	18503	32322	0.86	3.0E-01	AF229247.1	NT	Carigato orthopoxvirus hemagglutinin gene, complete cds
7175	19707	32555	0.78	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7367	19893	32758	6	3.0E-01	10947007	NT	Mus musculus midbrain (Midn-pending), mRNA
7512	20033	32899	1.88	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7867	20409	33318	1.07	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8314	20855		3.82	3.0E-01	8910101	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9f), mRNA
8411	20951	33870	1.27	3.0E-01	BE588083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8763	21302	34223	0.82	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactans isopenicillin N synthase (pcbc) gene, partial cds
8805	21344		0.95	3.0E-01	7661685	NT	Homo sapiens DKFZP680M0122 protein (DKFZP586M0122), mRNA
9145	21680	34624	0.88	3.0E-01	AF220507.1	NT	Anabaena POC7120 cytosine-specific DNA methyltransferase (dimB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9493	21963	34949	0.55	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9878	22375	35352	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288338 5'
10294	22788	35778	0.58	3.0E-01	AW118111.1	EST_HUMAN	xc03410.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808035 3'
10296	22790	35780	1.85	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BiP, complete cds
10315	22809	35801	0.73	3.0E-01	BF883841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5'
10315	22809	35802	0.73	3.0E-01	BF883841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5'
11604	24047	37112	2.87	3.0E-01	H51029.1	EST_HUMAN	yp84b10.t1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
11604	24047	37113	2.87	3.0E-01	H51029.1	EST_HUMAN	yp84b10.t1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
11975	24287		1.37	3.0E-01	PS4660	SWISSPROT	PONTICULIN PRECURSOR
12227	24884		2.93	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12529	25033		2.51	3.0E-01	6677788	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
1824	14509	27064	2.27	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2070	14650	27221	1.38	2.9E-01	AE000736.1	NT	Aquifex seductus section 68 of 109 of the complete genome
2524	15088		1.22	2.9E-01	M32360.1	NT	Mouse apolipoprotein A-II (Apo-2) gene, complete cds
3289	15900	28379	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-412 CT0328 Homo sapiens cDNA
3289	15900	28380	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-412 CT0328 Homo sapiens cDNA
3965	16563	29032	0.71	2.9E-01	A610836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4159	18751		0.67	2.9E-01	AW002802.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN) contains element L1 repetitive element;
4583	17166	28609	1.21	2.9E-01	AA284468.1	EST_HUMAN	wp02f10.x1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:2480395 3'
							z657d12.t1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4783	17372		0.63	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5148	17718		1.02	2.9E-01	U80756.1	NT	Lymnaea dispar vitellogenin gene, complete cds
5154	17724	30155	1.43	2.9E-01	7682169	NT	Homo sapiens KIAA0537 gene product (KIAA0537), mRNA
5285	17847		1.7	2.9E-01	AI870888.1	EST_HUMAN	vec08003.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2297308 3' similar to contains L1.12 L1 repetitive element;
5463	18098		1.25	2.9E-01	R37485.1	EST_HUMAN	y77612.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28281 3'
5582	19522	32344	0.79	2.9E-01	AF321001.1	NT	Sus scrofa domestica subsp. sassa S-adenosylmethionine synthetase 2 mRNA, complete cds
5837	18558	31286	5.1	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5837	18558	31286	5.1	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5849	18570	31302	6.06	2.9E-01	6678662	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6208	18816	31587	1.28	2.9E-01	AA418145.1	EST_HUMAN	z697612.r1 Soares NIHIMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6427	19030	31813	0.93	2.9E-01	AI797128.1	EST_HUMAN	wc27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.1 L1 repetitive element;
6487	19068	31854	2.3	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6585	19183	31983	0.72	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6585	19183	31984	0.72	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7082	18081	30437	1.35	2.9E-01	AF142329.1	NT	Mus musculus Flii protein (Flii) gene, complete cds; and Lfih protein (Lfih) gene, partial cds
7153	19885	32527	2.87	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPIER OXIDASE YDR508C
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; BING1 (BING1), tapasin (tapasin), RafGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
7213	19744	32598	1.61	2.9E-01	AF100958.1	NT	601085830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7860	20402	33308	1.82	2.9E-01	BE540422.1	EST_HUMAN	601085830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7860	20402	33309	1.82	2.9E-01	BE540422.1	EST_HUMAN	601085830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8103	20844		0.88	2.9E-01	BF217743.1	EST_HUMAN	601085830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4095113 5'
8531	21070	33990	0.68	2.9E-01	AI160910.1	EST_HUMAN	AU150810 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8856	21395	34318	1.07	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds
8963	21501	34423	0.71	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9170	21747	34688	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9170	21747	34690	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10773	23287	36302	2.24	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11041	23555	36589	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11041	23555	36590	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11453	23903	36970	2.07	2.9E-01	AA855373.1	EST_HUMAN	ny55902.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
11458	23906	36973	5.52	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
12172	24411	30944	1.64	2.9E-01	AW005671.1	EST_HUMAN	wz8805.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565621 3' similar to contains element
12262	24472	30832	1.47	2.8E-01	AF082453.1	NT	MER29 repetitive element;
12313	24505		1.4	2.9E-01	BE708189.1	EST_HUMAN	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12588	24679	30877	1.57	2.9E-01	Y08037.1	NT	601482050F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
12588	24679	30878	1.57	2.9E-01	Y08037.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
594	13224		2.06	2.8E-01	U67138.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
599	13228		0.75	2.8E-01	L28145.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1122	13725	26238	3.14	2.8E-01	AF168050.1	NT	Pruva dwarf virus movement protein, complete cds; coat protein, complete cds
1320	13914	26435	3.51	2.8E-01	BE313442.1	EST_HUMAN	Gura guira oocyte maturation factor Mos (c-mos) gene, partial cds
1320	13914	26436	3.51	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1334	13928	26448	1.03	2.8E-01	D86550.1	NT	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1765	14355	26902	2.01	2.8E-01	AW860020.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
2057	14638	27210	2.12	2.8E-01	AL047620.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2175	14752	27322	3.53	2.8E-01	AW511195.1	EST_HUMAN	DKFZp598I2321_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp598I2321
2511	15075	27648	2.41	2.8E-01	AE000494.1	NT	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2511	15075	27649	2.41	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2584	15147		2.75	2.8E-01	AL161565.2	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2688	15246	27813	1.21	2.8E-01	AB020975.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2688	15614		1.7	2.8E-01	AF179480.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2689	15615	28094	2.36	2.8E-01	Z14037.1	NT	Toxoplasma gondii 80kDa heat-shock protein (HSP90) mRNA, partial cds
2689	15615	28095	2.36	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3425	16033	28513	1.28	2.8E-01	AP000004.1	NT	B. taurus microsatellite (ETH121)
4068	16894	28125	2.06	2.8E-01	AE001180.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-884000 nt. position (477)
4202	16791		0.62	2.8E-01	AE004450.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4276	16882		2.75	2.8E-01	AE008888.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4553	-17136	29584	1.32	2.8E-01	AL021127.2	NT	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element/contains element MER22 repetitive element;
4559	17142	29590	2.47	2.8E-01	P13615	SWISSPROT	Mus musculus chromosome X contigA; putative Mages9 gene, Caltractin, NAD(P) ⁺ steroid dehydrogenase and Zinc finger protein 185
4887	17472	29628	1.07	2.8E-01	D15050.1	NT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
							Human mRNA for transcription factor AREB6, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4897	17472	29629	1.07	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4937	17512	29658	1.02	2.8E-01	AW594539.1	EST_HUMAN	hg68405.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2950569 3'
4949	17524	29685	1.17	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4955	17530	29672	3.5	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4986	17560	30003	1.67	2.8E-01	BF528186.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4180129 5'
5013	17587	30030	2.82	2.8E-01	AI272699.1	EST_HUMAN	gb86c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876028 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5514	24744	30558	21.59	2.8E-01	AA349697.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5781	18416	31132	2.78	2.8E-01	AB018025.1	NT	Homo sapiens OCTN2 gene, complete cds
5983	18603		0.97	2.8E-01	AW992583.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6078	18695	31442	0.69	2.8E-01	AA785286.1	EST_HUMAN	ca01d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK508-BINDING PROTEIN (HUMAN);
6323	25114		0.75	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6368	18970	31748	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6368	18970	31749	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6829	19419	32235	8.4	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B14-4d-4-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7467	19689		1.19	2.8E-01	U05633.1	NT	Maretea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7768	20276	33174	0.69	2.8E-01	BE537151.1	EST_HUMAN	601063105F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449568 5'
8036	20578	33482	1.12	2.8E-01	A1346128.1	EST_HUMAN	gp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1828289 3' similar to gb:X068323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8036	20578	33483	1.12	2.8E-01	A1346126.1	EST_HUMAN	gp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1828289 3' similar to gb:X068323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8150	20681	33605	2.18	2.8E-01	U51698.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8451	20991	33909	0.47	2.8E-01	AA911629.1	EST_HUMAN	cf02h05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M67769 IG
8525	21064		6.69	2.8E-01	BF347847.1	EST_HUMAN	GAMMA-1 CHAIN C REGION (HUMAN);
8987	21910	34761	1.22	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scn-2) gene, complete cds
9627	22127		1.03	2.8E-01	L13654.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
9803	22301	35286	1.04	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9803	22301	35287	1.04	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9861	22358	35338	0.84	2.8E-01	AF294393.1	NT	Rattus norvegicus glyceral-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
9972	22467	35451	1.91	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10215	22710		0.81	2.8E-01	8626154	NT	Fujinami sarcoma virus, complete genome
10255	22750	35738	0.47	2.8E-01	BE959727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639765 3'
10622	23154	36166	2.26	2.8E-01	BF241062.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10622	23154	36167	2.26	2.8E-01	BF241062.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10651	23183	36197	2.83	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
10760	23284	36297	3.31	2.8E-01	AF051682.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11158	23665		4.56	2.8E-01	BF974023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12213	24436		15.74	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12328	24514	30920	8.89	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0608-030400-001-e07 HT0608 Homo sapiens cDNA
12356	24533	30927	1.25	2.8E-01	BE800116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3655988 5'
12519	24988		2.21	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMIPK-like) (CDC42BPB), mRNA
502	13134	25622	3.21	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
641	13284	25740	2.53	2.7E-01	AA450061.1	EST_HUMAN	z39b10.s1 Soares_tet_Nb2H18_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1304	13898	26418	1.89	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element 1p100 gene for transposase, complete cds
1662	14255		2.17	2.7E-01	X79815.1	NT	G. lamblia SR2 gene
1767	14357	26903	3.34	2.7E-01	W56067.1	EST_HUMAN	z32h10.r1 Soares_fetal_Nb2H18 Homo sapiens cDNA clone IMAGE:341443 5'
1813	14403	26948	4.14	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2181	15459		2.77	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2405	14973	27545	7.35	2.7E-01	Y13688.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088P1U (M88), partial
2496	15060	27634	3.82	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NC1_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
3013	15629		0.73	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060800-385-e05 HT0875 Homo sapiens cDNA
4062	16678	29136	1.98	2.7E-01	AI928015.1	EST_HUMAN	w02a11.x1 NC1_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462828 3'
4096	16691	29147	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4096	16691	29148	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4101	16695	29151	2.31	2.7E-01	L177616.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5020	17594	30037	0.98	2.7E-01	L27616.1	NT	Triticum aestivum (W co68) gene, complete cds
5183	17758		3.82	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5471	18105	30424	2.07	2.7E-01	P17277	SWISSPROT	HOMEBOX PROTEIN HOXA-4 (CHOX-1.4)
5681	18308		0.86	2.7E-01	AB033171.1	NT	Astrocyte myelinophilin mitochondrial cytb gene for cytochrome b, partial cds
6724	19318	32122	1.07	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6724	18318	32123	1.07	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6875	18809	32443	2.03	2.7E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7085	18856	32495	0.76	2.7E-01	U15987.1	NT	Drosophila melanogaster rib-40 protein, Rop protein (Rop), and small GTP binding protein (DRac2) genes, complete cds
7383	18918	32782	0.87	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0583.3 IN CHROMOSOME X
7562	20079	32854	0.95	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7562	20079	32855	0.95	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7677	20188	33078	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7677	20188	33077	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7720	20228	33116	0.82	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7720	20228	33117	0.82	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7805	20348	33256	0.95	2.7E-01	AA013147.1	EST_HUMAN	ze35b11.s1 Soares retina N2b-4-IR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element
7989	20511		0.51	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8079	20621	33534	0.59	2.7E-01	AW868503.1	EST_HUMAN	MR1-SN0062-100500-002-d09 SN0062 Homo sapiens cDNA
8127	20668	33577	0.48	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8232	20773	33694	0.94	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8684	21233	34154	0.83	2.7E-01	Q14784	SWISSPROT	MAJOR VOLTAGE PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8957	21495	34418	0.53	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9256	21782	34734	9.83	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9256	21782	34735	9.83	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9259	21785		2.02	2.7E-01	P37828	SWISSPROT	FIMBRIAE W PROTEIN
9718	22214	35188	0.67	2.7E-01	D89680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9883	22488	35478	0.91	2.7E-01	AF081848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10028	22521	35517	2.5	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A7c isoform a (NF-A7c) mRNA, complete cds
10148	22843	35634	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10148	22843	35635	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10681	23221	36233	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10681	23221	36234	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10702	23231	36244	3.65	2.7E-01	AJ133268.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12298	24863		1.72	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12501	24627		3.98	2.7E-01	AF217491.1	NT	Homo sapiens fragile 18D alpha reductase (FOR) gene, exon 6
495	15416	25615	2.06	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
508	13139		1.24	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1437	14030	26558	2.19	2.6E-01	BE885087.1	EST_HUMAN	607510839F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1485	14078	26616	1.36	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1941	14525	27080	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1941	14525	27081	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb-M36072 605
							RIBOSOMAL PROTEIN L7A (HUMAN); gb-M14689_cds1 Mouse surfact locus surfact 3 protein gene (MOUSE);
2140	14718		13.12	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2197	14773	27347	1.41	2.6E-01	M11844.1	NT	B. maritimus rbcL gene
2512	15076		2.09	2.6E-01	Y12996.1	NT	607128018F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2960043 5'
2593	15146		10.77	2.6E-01	BE272440.1	EST_HUMAN	Bacteriophage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3640	16243	28719	0.86	2.6E-01	M22342.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5
3705	16306	28775	2.13	2.6E-01	AF228118.1	NT	EST371580 MAGE resequenced, MAGF Homo sapiens cDNA
4175	16766	29214	0.7	2.6E-01	AW959510.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4234	16822	29273	19.89	2.6E-01	BE080596.1	EST_HUMAN	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4448	17034	29477	1.57	2.6E-01	AF175293.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4593	17176	29622	0.76	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4593	17176	29623	0.76	2.6E-01	AB021180.1	NT	sa89d07.r1 Strabegene fetal retina B37202 Homo sapiens cDNA clone IMAGE:839477 5'
4846	17228	29684	1.35	2.6E-01	AA457817.1	EST_HUMAN	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3-1) mRNA, complete cds
4752	17333	29776	1.63	2.6E-01	U01103.1	NT	Ophrestia radiciosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4825	17403	29856	1.47	2.6E-01	AF142703.1	NT	yj51e06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:162288 5'
5107	17679	30118	3.56	2.6E-01	H04858.1	EST_HUMAN	em33b11.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5195	17760		0.58	2.6E-01	AA884625.1	EST_HUMAN	Parametrium caudatum gene for PAP, complete cds
5544	18176		1.29	2.6E-01	AB035972.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5840	18289	30742	0.68	2.6E-01	M96090.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6760	18388		0.81	2.6E-01	AI862388.1	EST_HUMAN	ts02a03.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2075768 3' similar to contains element MER35 repetitive element;
6847	18568	31289	0.89	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor (GHM enhancer 3 genes, partial cds; and unknown g>
8221	25113		2.38	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
8348	18953	31732	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q84288 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
8348	18953	31733	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q84288 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
8554	19182	31948	1.05	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 67
7103	18973	32512	0.97	2.6E-01	AI814380.1	EST_HUMAN	w448c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7457	24783		0.98	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 48
7721	20229	33118	1.6	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7791	20334	33240	1.14	2.6E-01	R02411.1	EST_HUMAN	y82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
7845	20387	33280	1.18	2.6E-01	BE144331.1	EST_HUMAN	MR0-HT0166-181198-003-412 HT0166 Homo sapiens cDNA
8083	20625	33538	0.67	2.6E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8083	20625	33539	0.67	2.6E-01	X82841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8276	20817	33738	2.99	2.6E-01	BF343588.1	EST_HUMAN	802014422F1 NCI_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4150398 5'
8349	20880	33810	1.89	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8627	21186	34080	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8627	21186	34081	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9388	21811	34762	0.96	2.6E-01	X17604.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
9654	22153		0.5	2.6E-01	AF057121.1	NT	Lentia canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9782	22280	35265	0.93	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
9782	22280	35268	0.93	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10083	22588		0.5	2.6E-01	Q28285	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10403	22897		0.81	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10500	22994		0.51	2.6E-01	AI978681.1	EST_HUMAN	wf58609.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491865 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11300	23762	36809	2.18	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11400	23851		30.88	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11777	24165		1.72	2.6E-01	10190855	NT	Mus musculus jerky (Jrk), mRNA
11973	24601		4.06	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12042	24329	30986	4.8	2.6E-01	AF316896.1	NT	Homo sapiens NaK-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced
12398	24556		1.34	2.6E-01	D88425.1	NT	Caenorhabditis elegans mRNA for serine/threonine kinase, complete cds
12478	24612		1.96	2.6E-01	AE001713.1	NT	Thermoboga maritima section 25 of 138 of the complete genome
12526	24641		1.37	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
12567	24666		3.74	2.6E-01	P47285	SWISSPROT	HYPOTHEITICAL PROTEIN MG039
262	12821	25407	1.48	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
263	12821	25407	1.77	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
276	12833		4.29	2.5E-01	M28501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
865	13480	25994	1.02	2.5E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1098	13703		1.03	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1160	13763	26274	11.59	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stratogene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1566	14156	26699	0.87	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1766	14356		6.09	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1827	15454	27087	1.29	2.5E-01	BE696804.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
1927	15454	27088	1.29	2.5E-01	BE696804.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
2452	15019		12.93	2.5E-01	AE000676.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2536	15100	27673	0.93	2.5E-01	6078216	NT	Mus musculus protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 (Pomt1), mRNA
2540	15104		1.49	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:684862 5'
3459	16066		3.41	2.5E-01	AW973471.1	EST_HUMAN	EST385484 IMAGE resequencer, MAGM Homo sapiens cDNA
3587	16191	28675	0.84	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3603	16207	28685	7.97	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4143	16735		1.36	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4409	16894		0.9	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4722	17303	28747	0.59	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds, and Naip3 gene, exons 2-9 and 11-16
4860	17438		1.47	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4889	17445	28898	4.69	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4890	17471	28927	2.82	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4924	17489		3.21	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MAERV-L (murine endogenous retrovirus) element
4959	17534	28976	0.61	2.5E-01	BE880785.1	EST_HUMAN	601437488F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'
5262	12933		0.65	2.5E-01	M26501.1	NT	Starfish (P ochraceus) cytoplasmic actin gene, complete cds
5529	18161	30576	12.86	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6114	18730		0.84	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6738	18332	32138	0.83	2.5E-01	AJ251973.1	NT	Homo sapiens partial steatrin-1 gene
7389	18914	32778	0.82	2.5E-01	U13892.1	NT	Feline calicivirus CFU68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene
7413	18938		1.35	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7632	20144	33025	4.48	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7786	20329	33236	2.31	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7797	20340	33248	0.7	2.5E-01	BE880712.1	EST_HUMAN	601683391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3820198 3'
8168	20709	33625	2.2	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862809 5'
8338	20877	33798	0.72	2.5E-01	P04482	SWISSPROT	ETB PROTEIN, SMALL T-ANTIGEN (ETB 18K)
8571	21110	34029	3.03	2.5E-01	H53236.1	EST_HUMAN	y84f07.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
8808	21347	34271	0.88	2.5E-01	M88828.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9435	21981	34909	15.98	2.5E-01	U88851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9435	21981	34910	15.98	2.5E-01	U88851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9492	21948	34887	2.09	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9492	21948	34888	2.09	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10010	22505	35498	1.68	2.5E-01	AW581987.1	EST_HUMAN	RC3-ST0188-130100-015-e07 ST0188 Homo sapiens cDNA
10438	22930	35937	1.53	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCL_CGAP_Uh1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
10439	22933	35941	1.31	2.5E-01	X59491.1	NT	Mouse L1Md LINE DNA
10459	22953	35962	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10459	22953	35963	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10955	23470	36495	4.3	2.5E-01	D50814.1	NT	Human mRNA for KIAA0124 gene, partial cds
11712	24122	37153	5.28	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
11740	25075		10.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
579	13209	25887	1.87	2.4E-01	AA836316.1	EST_HUMAN	on70d04.s1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582023 3'
881	13495	26014	2.4	2.4E-01	BF76124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1347	13942	28464	21.36	2.4E-01	AJ269880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1347	13942	28465	21.36	2.4E-01	AJ269880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1427	14020	28548	0.83	2.4E-01	Y17263.1	NT	Homo sapiens FLI-1 gene, partial
1801	14476	27277	27.27	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1944	14528	27084	1.17	2.4E-01	AF251708.1	NT	Zaocys diummedes fructose-1,6-bisphosphatase mRNA, complete cds
2079	14659	27230	1.49	2.4E-01	A1742958.1	EST_HUMAN	wg76405.x1 Soares NSF F8 gw OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:080267 KIAA0512 PROTEIN. ;
2183	14759	27328	1.04	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2213	14788	27451	1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2302	14875	27451	1.78	2.4E-01	AE000880.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2425	14893	27568	1.26	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI CGAP Cor16 Homo sapiens cDNA clone IMAGE:3318807 3' similar to SW.FRSB_XENLA
2575	15138	27708	3.05	2.4E-01	Z38534.1	NT	O42588 26S PROTEASE REGULATORY SUBUNIT 6A ;
2760	15343	27813	1.79	2.4E-01	X71783.1	NT	D. discoideum (A3-K) pona gene
2812	15364	27833	3.88	2.4E-01	AF030154.1	NT	S. pombe swi6 gene
3168	15780		3.27	2.4E-01	U72728.1	NT	Bovine adenovirus 3 complete genome
3182	15795	28267	1.39	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3724	16325	28792	1.26	2.4E-01	AF169793.1	NT	H. sapiens AGT gene, Pcd fragment of intron 4
3824	16424	28886	0.83	2.4E-01	AE000312.1	NT	Podospora anserina HET-C protein (Het-c) gene, complete cds
4103	16897		0.6	2.4E-01	D28680.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
5008	17581	30024	1.08	2.4E-01	AE000305.1	NT	Rattus norvegicus mRNA for alpha8 crystallin-related protein, complete cds
5220	17785	30203	0.93	2.4E-01	BE737592.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 195 of 400 of the complete genome
5302	17884		1.65	2.4E-01	K02402.1	NT	601572862F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3839775 5'
5653	18280	30758	0.83	2.4E-01	A825707.1	EST_HUMAN	Human coagulation factor IX gene, complete cds
5653	18280	30759	0.83	2.4E-01	A825707.1	EST_HUMAN	wc33405.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457128 3'
5676	18303	30785	0.85	2.4E-01	D50871.1	NT	wc33405.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457128 3'
5836	18480	31182	7.92	2.4E-01	AF081216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5836	18480	31183	7.92	2.4E-01	AF081216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
6050	24764		1.02	2.4E-01	AJ133838.2	NT	Mus musculus Wm protein (Wm) gene, complete cds
						NT	Branchiostoma floridae mRNA for calmodulin 2 (cam2 gene)
6054	18872	31411	2.38	2.4E-01	BF582338.1	EST_HUMAN	7154404.x1 NCI CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFRR4_HUMAN
6138	18752	31510	2.5	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGinine/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element ;
						NT	Drosophila melanogaster p38a MAP kinase gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	18949	31619	2.28	2.4E-01	7861801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6280	18898	31689	0.8	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cDAAD11.5'
6656	18252	32055	2.43	2.4E-01	AI698889.1	EST_HUMAN	wc82c11.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03484
7381	19007	32772	8.84	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7709	20218	33108	1.08	2.4E-01	AF228844.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8139	20680	33591	0.71	2.4E-01	AJ008397.1	NT	Mus musculus DDX48a protein (DDX48a) mRNA, complete cds
8139	20680	33592	0.71	2.4E-01	AJ008397.1	NT	Streptococcus pneumoniae r08 and h108 genes; two component system 08
8290	20831	33752	1.66	2.4E-01	AJ012585.1	NT	Streptococcus pneumoniae r08 and h108 genes; two component system 08
8535	21074	33994	0.97	2.4E-01	BF242794.1	EST_HUMAN	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8588	21127		0.58	2.4E-01	BF678275.1	EST_HUMAN	80187767F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106208 5'
9059	21598	34528	0.58	2.4E-01	AL138077.2	NT	802086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9059	21598	34527	0.58	2.4E-01	AL138077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9482	21881	34826	6.84	2.4E-01	AI693515.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
9620	22120	35083	0.8	2.4E-01	AF220067.1	NT	wk43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
9620	22120	35084	0.8	2.4E-01	AF220067.1	NT	MER22.b1 TAR1 repetitive element;
10335	22829	35823	1.95	2.4E-01	Q03682	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
10647	23179	36182	3.25	2.4E-01	AL161494.2	NT	Drosophila melanogaster SKPB gene, complete cds
10715	23243	36280	2.9	2.4E-01	AF030789.1	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11081	23583		2.28	2.4E-01	Z21847.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11665	24089	37145	1.91	2.4E-01	AF217491.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11807	24853		2.65	2.4E-01	AF004213.1	NT	P. asiatica mosaic virus genomic RNA
11868	24220		2.02	2.4E-01	AJ278191.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12086	24838		2.18	2.4E-01	V01507.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12320	25061		1.5	2.4E-01	BF229075.1	EST_HUMAN	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12562	24862		2.31	2.4E-01	AL163281.2	NT	Gallus gallus gene coding for a-actin
412	13047	25538	0.91	2.3E-01	U75898.1	NT	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
685	13289		4.4	2.3E-01	U97913.1	NT	Homo sapiens chromosome 21 segment HS21C081
695	13318	25803	17.02	2.3E-01	U67598.1	NT	aromatase [P.ophilus guttata=zabira finches, ovary, mRNA, 3188 nt]
968	13590	26092	3.44	2.3E-01	BE311893.1	EST_HUMAN	Mycoplasma genitalium section 35 of 51 of the complete genome
1847	14239	28774	1.19	2.3E-01	AJ245480.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
1674	14288	28800	2.75	2.3E-01	Y10887.2	NT	801142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3503818 5'
2089	14689		1.29	2.3E-01	AJ23533.1	NT	Brassica napus sig gene for S-b locus glycoprotein, cultivar T2
						NT	Mus musculus cdh5 gene, exon 1, partial
						NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	15054	27626	2.03	2.3E-01	BE287718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2678	15236	27803	1.16	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2651	14024	26552	1.42	2.3E-01	AB015033.1	NT	Marinibacteria agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2690	15606	28086	0.93	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THIR repetitive element;
3120	15734		6.96	2.3E-01	R21732.1	EST_HUMAN	Y121b07.s1 Soares, placenta Nb2-IP Homo sapiens cDNA clone IMAGE:130357 3'
3417	16025	28507	0.78	2.3E-01	H68836.1	EST_HUMAN	Y187h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3908	16507	28968	1.02	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4009	16607		5.14	2.3E-01	7682133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4442	17026	29468	0.83	2.3E-01	R82252.1	EST_HUMAN	Y17701.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:148017 5'
4489	17074		2.4	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4548	17131	28578	0.87	2.3E-01	D80989.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4586	17189	28613	2.16	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4652	17234	29690	6.13	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5180	17585	30028	0.82	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5202	17767	30191	0.62	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5403	17981	30372	0.9	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5507	18140	30552	2.39	2.3E-01	AB040845.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
6821	18250	30718	2.05	2.3E-01	BF058381.1	EST_HUMAN	7130b06.x1 NC1_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].
5721	18347	31050	4.58	2.3E-01	X86587.1	NT	C.familialis rom1 gene
5831	18455		1.19	2.3E-01	L39112.1	NT	Vitis vinifera corneum small subunit ribosomal RNA gene
6928	18648	31274	0.78	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2868 nt]
6986	18712	31461	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barslead aorta HPLR88 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6998	18712	31462	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barslead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6762	18355	32184	0.76	2.3E-01	AF198089.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
6859	19536	32360	4.1	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barslead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu repetitive element;
7185	19697	32544	0.7	2.3E-01	8823323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7331	19858	32721	0.69	2.3E-01	AF00227.1	NT	Secale cereale omega secalin gene, complete cds
7445	19889	32837	2.42	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7603	20116		3.63	2.3E-01	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
7608	20121	32998	1.63	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7732	20240		2.68	2.3E-01	N80893.1	EST_HUMAN	zrl2a08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:292358 5'
7783	20338	33243	0.58	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
7835	20477	33387	1.83	2.3E-01	M88831.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8430	20970	33882	0.6	2.3E-01	U57899.1	NT	Mus musculus prosaposin (psapSGP-1) gene, complete cds
9087	21804	34534	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST84081 Rhadomyosarcoma Homo sapiens cDNA 5' and similar to DnaJ homolog (GB:X633388)
9087	21804	34535	0.87	2.3E-01	AA372184.1	EST_HUMAN	EST84081 Rhadomyosarcoma Homo sapiens cDNA 5' and similar to DnaJ homolog (GB:X633388)
9501	22001	34958	0.65	2.3E-01	8678318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
9644	22144	35112	0.51	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2968739 5'
9697	22198	35169	0.78	2.3E-01	AW964460.1	EST_HUMAN	EST7376533 MAGE resequences, MAGE1 Homo sapiens cDNA
9746	22244	35225	1.22	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9781	22279	35284	0.55	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281299-001-04 DT0036 Homo sapiens cDNA
9847	22345	35326	2.6	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
9803	22400	35373	1.83	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10339	22833	35828	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22845		5.86	2.3E-01	BF133577.1	EST_HUMAN	60184615R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10893	23414	36432	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10893	23414	36433	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11068	23580	36619	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein S34 (mg534 gene)
11068	23580	36620	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein S34 (mg534 gene)
11230	23781	36817	2.49	2.3E-01	AE002187.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
11624	24066		1.6	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11788	24172		2.82	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
11878	24226		57.94	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M8 Homo sapiens cDNA clone HCOE44 5'
11899	24804		1.31	2.3E-01	AA089819.1	EST_HUMAN	chh1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
11908	24240		1.61	2.3E-01	AW803940.1	EST_HUMAN	PIMA-SIN0012-030400-001-006 SIN0012 Homo sapiens cDNA
11969	25002	30810	3.1	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q82175 Q82175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	RF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12007	25053	30511	10.98	2.3E-01	BE882484.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3308689 5'
12057	24340		1.94	2.3E-01	BF063319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4287719 5'
12107	24369		3.11	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12205	24429		1.36	2.3E-01	U48945.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12211	24369		1.67	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12490	24614		2.67	2.3E-01	BF476811.1	EST_HUMAN	nec30h12x1 Lupski_sclafic_nerve Homo sapiens cDNA clone IMAGE:3305950 3' similar to contains element
12608	24898	30710	1.26	2.3E-01	AA094108.1	EST_HUMAN	MER38 repetitive element
83	12769	25252	0.91	2.2E-01	AI052190.1	EST_HUMAN	c1894.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
1611	14204	28738	2.85	2.2E-01	AF167850.1	NT	oz14a10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
2063	14643		3.89	2.2E-01	AF171801.1	NT	TR:Q13040 Q13040 A TP-BINDING CASSETTE PROTEIN ;
2136	14714	27287	3.16	2.2E-01	M34840.1	NT	Homo sapiens PPAR delta gene, promoter region
2447	15014	27588	5.61	2.2E-01	BF677638.1	EST_HUMAN	Timenesurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2623	15185	27751	1.27	2.2E-01	BE618258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2623	15185	27752	1.27	2.2E-01	BE618258.1	EST_HUMAN	602085603F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5'
2703	15260		1.17	2.2E-01	AL163218.2	NT	601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3898190 5'
2906	15523	27983	4.28	2.2E-01	BE155625.1	EST_HUMAN	601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3898190 5'
2906	15523	27984	4.28	2.2E-01	BE155625.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
2947	15563		1.04	2.2E-01	AF020503.1	NT	PM2-HT0353-281289-003-a12-HT0353 Homo sapiens cDNA
3439	16047		2.67	2.2E-01	AL161562.2	NT	PM2-HT0353-281289-003-a12-HT0353 Homo sapiens cDNA
3896	16484		1.18	2.2E-01	AF156728.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4291	16877		1.26	2.2E-01	AF119102.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4300	16886	28330	7.03	2.2E-01	AF155142.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4350	16937	28378	2.59	2.2E-01	AF117340.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4350	16937	28379	2.59	2.2E-01	AF117340.1	NT	Mus musculus ribbed lineage kinase 3 (Mlck3) and two pore domain K+ channel subunit (Kcnid6) genes, complete cds
4447	17033	29475	1.36	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4447	17033	29476	1.36	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4952	17527		1.35	2.2E-01	D50804.1	NT	Human scRNA (BC200 beta) pseudogene
4957	17532	28974	2.86	2.2E-01	AA211216.1	EST_HUMAN	Human beta-cytoplasmic actin (ACTBP9) pseudogene
5198	17781		1.33	2.2E-01	L13289.1	NT	zq87c05.r1 Streptococcus NNT neuron (8837233) Homo sapiens cDNA clone IMAGE:648988 5'
5203	17788		1.79	2.2E-01	AE001137.1	NT	Mus musculus vinculin gene, exon 3
							Borrelia burgdorferi (section 23 of 70) of the complete genome

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5281	17853	30277	1.2	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0067-201089-002-c10 HT0067 Homo sapiens cDNA
5316	17878		0.9	2.2E-01	S57565.1	NT	histamine H2-receptor [rats, Genomic, 1928 nt]
5919	18541	31267	2.46	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 158, mRNA
5930	18552		3.53	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2639899
6150	18763	31525	0.73	2.2E-01	U97087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6150	18763	31526	0.73	2.2E-01	U97087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6807	19388	32212	0.85	2.2E-01	AB038480.1	NT	Homo sapiens gene for fukutin, complete cds
7093	19684	32503	9.14	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAH008 5'
7183	19715	32562	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spaA) genes, complete cds; and unknown genes
7183	19715	32563	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spaA) genes, complete cds; and unknown genes
7333	19860	32723	2.01	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
7333	19860	32724	2.01	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
7688	20197	33085	0.68	2.2E-01	AF287987.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7963	20505		3.06	2.2E-01	AF155143.1	NT	Mus musculus rrm23-M1 gene, promoter region
8032	20574	33479	0.84	2.2E-01	Z49933.1	NT	E.coli sepA and sepB genes
8815	21354	34277	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8815	21354	34278	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8827	21368	34290	3.48	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
8847	21388	34310	1.02	2.2E-01	U09884.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
8952	21490		3.12	2.2E-01	AW85039.1	EST_HUMAN	PM9-CT0263-241289-008-b07 CT0263 Homo sapiens cDNA
9043	21580	34509	1.82	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9126	21661	34804	1.95	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9213	21730	34873	1.24	2.2E-01	W02988.1	EST_HUMAN	zod4f08.1 Soares melanocyte ZN4HM Homo sapiens cDNA clone IMAGE:291581 5'
9231	21953	34903	14.03	2.2E-01	P49834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9274	21800	34750	0.74	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xldp3)
9285	21855	34830	0.71	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9288	21868	34845	3.69	2.2E-01	M89643.1	NT	Brachydanio rerio opandymin beta and gamma chains (Epd) gene, complete cds
9639	22039	35000	0.59	2.2E-01	Q90860	SWISSPROT	CYCLOC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9729	22227	35204	3.1	2.2E-01	AF197841.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPaHSP21) mRNA, complete cds; nuclear gene for chloroplast product
9864	22361	36341	2.23	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10079	22674	36568	0.87	2.2E-01	6825671	NT	Human herpesvirus 5, complete genome
10340	22834		0.61	2.2E-01	AF071001.1	NT	Mus musculus PIR1 (Pir1) gene, partial cds
10384	22878	36870	0.72	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10384	22878	36871	0.72	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11005	23519	36554	1.8	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11299	23751	36808	5.58	2.2E-01	X01818.1	NT	Drosophila 68C glue gene cluster
11335	23033	36042	3.18	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
11715	24125		1.8	2.2E-01	BE870859.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
11827	25065		6.34	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
11910	24248		5.37	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12024	18029	30491	1.7	2.2E-01	AW361088.1	EST_HUMAN	RC1-CT0249-141189-021-g04 CT0249 Homo sapiens cDNA
12026	24317		1.85	2.2E-01	AW681822.1	EST_HUMAN	h17602.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
12575	25058		4.05	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5'
12659	24730	30855	2.44	2.2E-01	BF243095.1	EST_HUMAN	601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104988 5'
1008	13617	26132	1.38	2.1E-01	AA569289.1	EST_HUMAN	mm31e11.s1 NCL_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061804
1009	13619	26134	1.27	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1163	13765		2.41	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1240	13838	26354	0.85	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1240	13838	26355	0.85	2.1E-01	6754289	NT	Mus musculus mas proto-oncogene and lig2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1557	14149	26681	3.45	2.1E-01	AJ246895.1	NT	Mus musculus mas proto-oncogene and lig2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1957	14541	27097	1.84	2.1E-01	AA906824.1	EST_HUMAN	ck73s02.s1 NCL_CGAP_GCA1 Homo sapiens cDNA clone IMAGE:1518810 3' similar to gb:K02765
2201	14777	27350	3.39	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN).
2385	14954	27526	2.01	2.1E-01	6753235	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2385	14954	27526	2.01	2.1E-01	6753235	NT	Mus musculus calcium channel, voltage dependent, alpha2/delta subunit 3 (Ca _v 2d3), mRNA
2361	15667	28041	2.53	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (seg-related), member 4 (KCNH4), mRNA
3879	16477		6.58	2.1E-01	6838361	NT	Beta vulgaris mitochondrion, complete genome
4129	16721	26176	1.22	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4129	16721	29177	1.22	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4338	16823		1.38	2.1E-01	AF124528.1	NT	Orchestria cawiana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4405	17051		1.51	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4678	17258	29709	1.83	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
5083	17656	30097	1.83	2.1E-01	U78409.1	NT	Lycopodium esculentum homeobox 1 protein (THor1) mRNA, partial cds
5434	17860	30398	0.88	2.1E-01	U05082.1	NT	Vampire bat (D. rotundus) plasminogen activator mRNA, complete cds
5504	18138	30548	6.55	2.1E-01	BF672606.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6267	18544	32368	1.16	2.1E-01	AJ223392.1	NT	Dodo fragilis mitochondrial 16S rRNA gene, partial
6978	19477	32289	2.04	2.1E-01	U04942.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7438	19890	32825	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7438	19890	32826	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7447	19971		2.17	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7692	20201	33088	2.02	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7731	20239	33130	1.14	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7731	20239	33131	1.14	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7765	20273		0.88	2.1E-01	T87354.1	EST_HUMAN	y883b01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114783 5'
8017	20559		1.19	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8439	20979	33894	4.93	2.1E-01	U68389.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8732	21271	34180	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H0814 5'
8732	21271	34191	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H0814 5'
8888	21428		0.47	2.1E-01	AB022524.1	NT	Homo sapiens APCL gene, exon 9
8987	21505	34428	5.93	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
9423	21932	34890	0.6	2.1E-01	N42536.1	EST_HUMAN	Y11e10.r1 Soares melanocyte 2NBM-Homo sapiens cDNA clone IMAGE:270654 5'
9423	21932	34891	0.6	2.1E-01	N42536.1	EST_HUMAN	Y11e10.r1 Soares melanocyte 2NBM-Homo sapiens cDNA clone IMAGE:270654 5'
9432	21958	34908	2.95	2.1E-01	X97378.1	NT	A. thaliana mRNA for AFRanBP1b protein
9536	22036	34998	1.57	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10232	22727	35718	1.04	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10283	22758	35745	1.96	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10289	22764	35751	0.67	2.1E-01	BF574254.1	EST_HUMAN	(80 KD DIACYLGLYCEROL KINASE) 602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10505	22389	36007	0.5	2.1E-01	AF294296.1	NT	Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11438	23898		2.24	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11451	23901	36969	2.34	2.1E-01	BE180422.1	EST_HUMAN	RC3-H10822-040500-013-b11 HT0822 Homo sapiens cDNA
11641	24602		1.39	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12163	24418		1.46	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12465	24593		1.72	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'
12607	24691	30856	2.08	2.1E-01	BE672330.1	EST_HUMAN	765602x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3223034 3'
12612	24695	30861	1.26	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
214	12875	25362	1.96	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
559	13190		2.2	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
728	13348	25940	1.24	2.0E-01	MT7085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
843	13459	25968	1.76	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1049	13656	26167	0.72	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7127, 761449-620916
1164	13766	26276	3.24	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1267	13891	26414	1.37	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1351	13946	26470	1.22	2.0E-01	AW384637.1	EST_HUMAN	PM1-HT0422-291290-002-c06 HT0422 Homo sapiens cDNA
1507	14099		1.22	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1534	14126	26663	23.08	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1569	14191	26722	3.03	2.0E-01	AB007674.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1604	14196	26728	1.23	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1735	14326	26868	1.17	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14345		1.83	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1795	14365		1.99	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1834	14518	27073	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1934	14518	27074	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1837	14521	27077	1	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2366	14955		1.84	2.0E-01	X62877.1	NT	H. sapiens Nar-D-glucose cotransport regulator gene
2915	15532		0.66	2.0E-01	AF074900.1	NT	Homo sapiens full length insert cDNA YH85A11
3534	16139	26621	0.7	2.0E-01	P46907	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3626	16229		0.82	2.0E-01	AW238005.1	EST_HUMAN	xp15602x1 NCI_CGAP_HNB Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3768	16369	26635	0.8	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ; CED-11 PROTEIN

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
4028	16626	29098	0.78	2.0E-01	NT	<i>Sus scrofa</i>
4102	16668	29152	0.68	2.0E-01	NT	<i>C.parastifica</i> capC gene
4522	17108	29552	0.78	2.0E-01	NT	<i>Mus musculus</i> neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-18
4865	17247		8.43	2.0E-01	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5192	17757	30188	7.09	2.0E-01	8822080	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5228	16139	29821	0.62	2.0E-01	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5638	18265	30737	2.38	2.0E-01	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5916	18538	31283	2	2.0E-01	11432540	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6008	18628	31361	0.69	2.0E-01	X91856.1	<i>F.rubripes</i> DNA encoding for vely-RNA synthetase
6210	18820	31591	6.48	2.0E-01	U15300.1	<i>Saccharomyces cerevisiae</i> Hef5p (HAL5) mRNA, complete cds
6321	18928		0.71	2.0E-01	M75967.1	Human hepatocyte growth factor gene, exon 1
6560	19158	31955	3.94	2.0E-01	X61033.1	<i>M.aureus</i> mu class glutathione transferase gene
6650	19246	32049	3.63	2.0E-01	AW360865.1	PM1-CT0247-141098-001-g08 CT0247 Homo sapiens cDNA
7251	19780	32838	0.68	2.0E-01	U93724.1	<i>Mycoplasma genitalium</i> section 46 of 51 of the complete genome
7338	19893	32727	1.18	2.0E-01	AF260371.1	<i>Mus musculus</i> phosphofructokinase-1 C isozyme (Pfkc) gene, exons 3 through 7
7775	20284	33181	1.53	2.0E-01	AK024427.1	Homo sapiens mRNA for FLJ00016 protein, partial cds
7895	20437		8.45	2.0E-01	AF028028.1	Andes virus strain O423133 glycoprotein G1 and G2 precursor, gene, partial cds
8142	20683	33596	2.91	2.0E-01	X91151.1	<i>M.musculus</i> scp2 gene exon 14
8858	21197		0.53	2.0E-01	BE562247.1	601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677784 5
9273	21789	34749	1.03	2.0E-01	U82511.1	<i>Dicotyledonum discoidium</i> random slug cDNA19 protein (rsc19) mRNA, partial cds
9312	21828	34775	0.66	2.0E-01	U71122.1	<i>Arabidopsis thaliana</i> pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9475	21874		4.35	2.0E-01	AE001278.1	<i>Chlamydia trachomatis</i> section 5 of 87 of the complete genome
9681	22160	35132	0.51	2.0E-01	P11420	DAUGHTERLESS PROTEIN
9681	22160	35133	0.51	2.0E-01	P11420	DAUGHTERLESS PROTEIN
9808	22304		1.88	2.0E-01	AF146992.1	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9854	22449	35431	1.78	2.0E-01	AF086907.1	<i>Arabidopsis thaliana</i> root gravitropism control protein (PIN2) gene, complete cds
9854	22449	35432	1.79	2.0E-01	AF086907.1	<i>Arabidopsis thaliana</i> root gravitropism control protein (PIN2) gene, complete cds
10072	22567	35562	0.53	2.0E-01	AF157814.1	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10072	22567	35563	0.53	2.0E-01	AF157814.1	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10115	22610		0.72	2.0E-01	X78398.1	<i>D.melanogaster</i> DNA mobile element (hoppe)
10304	22798	35789	0.88	2.0E-01	X97121.1	<i>R.norvegicus</i> mRNA for NTR2 receptor
10720	23248	36263	2.77	2.0E-01	D89088.1	<i>Salvelinus pluvius</i> mRNA for transferrin, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10720	23248	30284	2.77	2.0E-01	D80888.1	NT	Sarvelinus pluvius mRNA for transferrin, complete cds
12182	24402		1.34	2.0E-01	AF208837.2	NT	Pimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12374	24887		1.95	2.0E-01	AF302773.1	NT	Homo sapiens nitrin-Lm isoform (nitrin) mRNA, complete cds
12388	24807	30788	2.81	2.0E-01	AW975287.1	EST_HUMAN	EST387405 IMAGE resequences, MAGN Homo sapiens cDNA
12425	24810	30888	3.97	2.0E-01	A023582.1	EST_HUMAN	ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12449	24584		17.06	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
115	12786		6.22	1.8E-01	7548743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
374	13023	25509	5.4	1.8E-01	AF004353.1	NT	Mus musculus pelle ear (ep) gene, wild type allele, 3' region, partial cds
684	13308	25792	1.47	1.8E-01	U32581.2	NT	Homo sapiens lambda106 protein kinase C-interacting protein mRNA, complete cds
684	13308	25793	1.47	1.8E-01	U32581.2	NT	Homo sapiens lambda106 protein kinase C-interacting protein mRNA, complete cds
691	13315	25800	6.6	1.8E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
692	13315	25800	6.82	1.8E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
1023	13633		1.92	1.8E-01	7305180	NT	Mus musculus interauctin 2 receptor, gamma chain (Il2rg), mRNA
1143	13748	26258	10.04	1.8E-01	A4358813.1	EST_HUMAN	EST87784 Fetal lung II Homo sapiens cDNA 5' end
1413	14006	26534	2.41	1.8E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1482	14075		4.02	1.8E-01	AF184823.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2185	14761	27331	1.29	1.8E-01	AA916482.1	EST_HUMAN	d44H09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1528368 3' similar to gb:AC03911
2422	14990	27583	3.27	1.8E-01	8822533	NT	GLIA DERIVED NEXIN PRECURSOR (HUMAN);
2949	15565	28039	4.1	1.8E-01	U68068.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2965	15590		6.58	1.8E-01	J00822.1	NT	Sigmoidon hispidus p53 gene, partial cds
3033	15649	28128	1.05	1.8E-01	U25148.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3442	16050	28528	4.19	1.8E-01	D13197.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3528	16131	28611	5.24	1.8E-01	R16467.1	EST_HUMAN	Mouse gene for immunoglobulin diversity region D1
3877	16475	28939	0.76	1.8E-01	AF284017.1	NT	y4210.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
4084	16681	29123	3.85	1.8E-01	AB006784.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4157	16749	29202	1.86	1.8E-01	AW754106.1	EST_HUMAN	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4315	16901	29345	1.17	1.8E-01	BE834943.1	EST_HUMAN	CM3-CT0315-271189-045-b11 CT0315 Homo sapiens cDNA
4588	17161	29587	0.69	1.8E-01	AL161483.2	NT	MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
5153	17728		1.11	1.8E-01	AF223842.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5789	18414		5.46	1.8E-01	AW130149.1	EST_HUMAN	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5828	18450	31173	7.81	1.8E-01	AF127837.1	NT	x728a07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2819444 3' similar to gb:M73779 RETINOIC
6005	18625	31360	0.73	1.8E-01	AF091216.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
							Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
							Mus musculus Wm protein (Wm) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6046	18695		2.52	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6469	19070	31855	1.07	1.9E-01	A1762391.1	EST_HUMAN	w54h02.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2394098 3'
6623	19123	31916	1.23	1.9E-01	AW148462.1	EST_HUMAN	xf14c08.x1 NCI_CGAP_K148 Homo sapiens cDNA clone IMAGE:2818030 3' similar to gb:X035559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7050	18068	30460	1.37	1.9E-01	R43212.1	EST_HUMAN	y08a12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7072	19844	32481	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7072	19844	32482	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7503	20025	32989	1.3	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7543	20083	32937	2.89	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
7827	20488	33378	1.71	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8820	21159	34074	12.12	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8875	21414	34337	1.38	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8875	21414	34338	1.38	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9789	22287	35271	0.72	1.9E-01	AA912486.1	EST_HUMAN	cd9g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element
10140	22635	35628	0.71	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10140	22635	35627	0.71	1.9E-01	BE830353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10523	23081	36071	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10523	23081	36072	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10835	23187	36178	2.08	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11377	23828	36891	1.68	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11571	24018	37088	2.69	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12207	24431		1.33	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
12582	24874		3.69	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
34	12713	25172	2.56	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
281	15412	25423	1.67	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
383	13039	25530	1.76	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
776	13396	25996	0.77	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1018	13628	26141	0.78	1.8E-01	A1912212.1	EST_HUMAN	wd7102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1130	13732	26242	1.28	1.8E-01	AF000580.1	NT	Dicotyledon discoidium plasmid Ddp5, complete genome
1332	13928	26447	6.97	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1551	14143	28678	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1551	14143	28677	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1887	14472		2.79	1.8E-01	4505038	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1907	14492		2.22	1.8E-01	A1733708.1	EST_HUMAN	cg22ad10.x6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1781811 3' similar to TR:O76838 O76838 GAMMA BUTYROBETAINE HYDROXYLASE:
1958	14542	27088	1.52	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2718	15273		2.28	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081289-036-p04 DT0018 Homo sapiens cDNA
2923	15540		2.36	1.8E-01	AF194589.1	NT	Jonopsidium aculea LEAFY protein (LEAFY2) gene, partial cds
2828	15544	28020	1.18	1.8E-01	AW182300.1	EST_HUMAN	X41403.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2859756 3'
3158	15772	28238	1.31	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3413	16021	28501	0.71	1.8E-01	BF183582.1	EST_HUMAN	601809/23R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3683	16284	28752	0.79	1.8E-01	H033389.1	EST_HUMAN	X45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3683	16284	28753	0.79	1.8E-01	H033389.1	EST_HUMAN	X45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4333	16920	28382	0.78	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4428	17012		4.07	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BdA-DQB), complete cds
4654	17236	28691	6.59	1.8E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
4898	17461	28914	2.51	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4928	17503	28950	1.03	1.8E-01	X82179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
5198	17763	30188	2.18	1.8E-01	AW814270.1	EST_HUMAN	MR9-ST0203-151289-112-p08 ST0203 Homo sapiens cDNA
5216	17781	30200	1.59	1.8E-01	A17922382.1	EST_HUMAN	an28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5257	17820	30245	1.5	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5281	17843	30270	1.07	1.8E-01	A1439881.1	EST_HUMAN	157804.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5298	17850	30276	0.59	1.8E-01	AF132115.1	NT	Arabidopsis thaliana cytochrome b-561 (CYTB561) gene, partial cds
5338	17899	30314	0.78	1.8E-01	AJ132844.1	NT	Broad bean with virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5338	17899	30315	0.78	1.8E-01	AJ132844.1	NT	Broad bean with virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5398	17956	30367	2.04	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST0121-041189-019-b01 ST0121 Homo sapiens cDNA

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5976	18598	31331	1	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6082	18689	31448	1.01	1.8E-01	N28629.1	EST_HUMAN	y438h08.l1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:284063 5'
6277	18885	31653	1.1	1.8E-01	6878428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6277	18885	31654	1.1	1.8E-01	6878428	NT	Mus musculus Trif receptor-associated factor 6 (Trif6), mRNA
6635	19231	32035	2.03	1.8E-01	Q8QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6875	19271		2.24	1.8E-01	N94893.1	EST_HUMAN	y462h02.l1 Soares multiple sclerosis 2N1bHMS Homo sapiens cDNA clone IMAGE:278163 5'
7077	19649	32487	1.22	1.8E-01	AB018561.1	NT	Citrus limonius mRNA for vsus, complete cds
7077	19649	32488	1.22	1.8E-01	AB018561.1	NT	Citrus limonius mRNA for vsus, complete cds
7117	19457	32272	0.71	1.8E-01	BE681853.1	EST_HUMAN	601848361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
8547	21088	34009	0.47	1.8E-01	AW966118.1	EST_HUMAN	EST378101 MAGE resequences, MAGI Homo sapiens cDNA
9268	21782	34741	1.13	1.8E-01	MF3258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9298	21896	34843	1.39	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9412	21921		0.55	1.8E-01	AA463751.1	EST_HUMAN	h02a05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:949088 similar to contains L1.13 L1
9494	21994	34950	1.13	1.8E-01	P15272	SWISSPROT	repetitive element;
9494	21994	34951	1.13	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9532	22032	34980	0.95	1.8E-01	M26019.1	NT	AMP NUCLEOSIDASE
9532	22032	34991	0.95	1.8E-01	M26019.1	NT	S. commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9894	22193	35168	0.62	1.8E-01	P08123	SWISSPROT	S. commune oridine-5'-phosphate decarboxylase (URA1) gene, complete cds
9898	22197	35170	0.69	1.8E-01	U67548.1	NT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10039	22534		0.64	1.8E-01	AF200262.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome product
10271	22766	35753	1.22	1.8E-01	X63440.1	NT	Aquarius emplus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial
10516	23054	36068	2.37	1.8E-01	X77338.1	NT	product
10558	23094	36106	7.47	1.8E-01	U38906.1	NT	Mus musculus mRNA for P19-protein tyrosine phosphatase
10615	19649	32487	3.07	1.8E-01	AB018561.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10615	19649	32488	3.07	1.8E-01	AB018561.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysis genes, complete cds
10618	23148	36160	4.49	1.8E-01	AF019107.1	NT	Citrus limonius mRNA for vsus, complete cds
10897	23417	36434	1.84	1.8E-01	M56257.1	NT	Citrus limonius mRNA for vsus, complete cds
11337	23035	36045	4.3	1.8E-01	X57033.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
11589	24042	37111	2.74	1.8E-01	8394421	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11626	24068	37132	1.8	1.8E-01	U40487.1	NT	B. taurus mRNA for potassium channel
11748	24148		2.04	1.8E-01	10086561	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
							Mycobacterium smegmatis proton antiporter efflux pump (lfrA), complete cds
							Bovine ephemeral fever virus, complete genome

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11814	24188	31032	1.41	1.8E-01	BF348823.1	EST_HUMAN	602010828F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4155318 5'
12218	13828	28447	1.3	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12291	24481		5.61	1.8E-01	Q86882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN)
12416	24689		23.47	1.8E-01	R24494.1	EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12459	24590		2.75	1.8E-01	Y11114.1	NT	E. dispar mRNA for headkinase (hok1)
12502	25045	30507	1.58	1.8E-01	6508952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcedoa), mRNA
603	13232	25705	5.53	1.7E-01	BE385184.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815788 5'
838	13454	25884	2.89	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
988	13608		8.63	1.7E-01	P35816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1088	13701	28210	0.87	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1098	13701	28211	0.87	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1853	14441	26898	0.85	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
2025	14807		2.84	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2885	15503	27873	1.98	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2886	15503	27874	1.98	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2953	15569	28044	1.53	1.7E-01	AA336808.1	EST_HUMAN	EST41851 Endometrial tumor Homo sapiens cDNA 5' end
3027	15643	28121	1.9	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3027	15643	28122	1.9	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3138	15753	28220	1.91	1.7E-01	AF081514.1	NT	Tecus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3412	16020	28500	1.11	1.7E-01	N55763.1	EST_HUMAN	J2348F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2348 5'
3494	16099	28574	1.26	1.7E-01	AJ288505.1	NT	Arabidopsis sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4012	16610	29083	4.89	1.7E-01	AJ253377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4658	17240		1.63	1.7E-01	X52836.1	NT	Schistosoma gregaria alpha repetitive DNA
4877	17452	28804	0.84	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D cdc10 reductase (FOR) gene, exons 8, 9, and partial cds
4965	17539	28981	1.07	1.7E-01	AI247635.1	EST_HUMAN	qhs7c08.x1 Soares fetal liver spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.01 ORF repetitive element
5210	17775		0.88	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5242	17808	30227	1.02	1.7E-01	BF688719.1	EST_HUMAN	602186830F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288848 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5297	17959		1.08	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (se) gene, complete cds
5342	17903	30319	0.8	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5421	17978	30388	7.82	1.7E-01	U04479.1	NT	S.pneumoniae DNA polymerase I (polA) gene, complete cds
5604	18233	30683	1.92	1.7E-01	AA470886.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17888 60S
5804	18233	30684	1.92	1.7E-01	AA470886.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17888 60S
5779	18404	31120	0.7	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6471	19072	31858	20.9	1.7E-01	H72118.1	EST_HUMAN	ys02p08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:213658 3'
6522	19122	31913	1.33	1.7E-01	A1370978.1	EST_HUMAN	la20c11.x1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6522	19122	31914	1.33	1.7E-01	A1370978.1	EST_HUMAN	la20c11.x1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6837	18045	30467	0.71	1.7E-01	BE300286.1	EST_HUMAN	600844087T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3'
6860	19537		2.28	1.7E-01	AF028652.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7074	19848		0.67	1.7E-01	Z82910.1	NT	Homo sapiens HFE gene
7272	19800	32657	2.83	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7339	19898	32730	8.92	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7494	20017	32882	1.16	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7508	24784	32893	0.73	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
7802	20345	33253	1.26	1.7E-01	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
7904	20446	33352	0.54	1.7E-01	AF150689.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8219	20760	33874	6.62	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8219	20760	33875	6.62	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8631	21170	34087	0.58	1.7E-01	AW982873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8682	21201	34119	3.28	1.7E-01	D00394.1	NT	Rat (SHR strain) SX1 gene
8778	21317	34239	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8778	21317	34240	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9095	21631	34569	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9095	21631	34570	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9509	22009	34867	7.72	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9814	22114	35077	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGO ressequences, MAGO Homo sapiens cDNA
9814	22114	35078	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGO ressequences, MAGO Homo sapiens cDNA
9831	22131	35098	2.47	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9704	22203	35174	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9704	22203	35175	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9722	22220	35105	0.81	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp8 gene)
10132	22627		2.24	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10263	22787	35777	0.99	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10286	22789	35779	1.72	1.7E-01	AA827972.1	EST_HUMAN	ng90a07.s1 NCI CGAP_C08 Homo sapiens cDNA clone IMAGE:1148282 3' similar to gb:L25081
10560	23098	36109	9.23	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
10665	23215	36227	2.63	1.7E-01	AA814817.1	EST_HUMAN	801286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
10891	23505	36536	8.7	1.7E-01	7108300	NT	d43a03.s1 NCI CGAP_QNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
10891	23505	36537	8.7	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA
11558	24008		2.18	1.7E-01	P15272	SWISSPROT	Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA
11643	24004		1.45	1.7E-01	AJ272584.1	NT	AMP NUCLEOSIDASE
11647	24079	37143	4.09	1.7E-01	11418157	NT	Blibella aurantiaca mitochondrial partial COII gene for cytochrome c oxidase subunit II
11782	25004		1.94	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CAGNA1I), mRNA
12333	24517		1.38	1.7E-01	N40825.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
12361	24548	30805	12.95	1.7E-01	U01317.1	NT	yw62c12.r1 Soares_placenta_8to9weeks_2NHIP8a8W Homo sapiens cDNA clone IMAGE:258742 5'
12609	24683		1.33	1.7E-01	AJ132510.1	NT	Human beta globin region on chromosome 11
131	12738	25285	1.57	1.6E-01	AF217532.1	NT	Sus scrofa c-fos gene, exons 1-4
708	15388	25816	1.56	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1569	14161	26862	4.35	1.6E-01	AF298117.1	NT	yh75f12.r1 Soares_placenta_Nb2f4P Homo sapiens cDNA clone IMAGE:135589 5'
1968	14552	27108	2.8	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
2028	14610		1.08	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2427	15468	27569	0.98	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2535	15089	27672	1.12	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2917	15534	28008	11.95	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2917	15534	28007	11.95	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3041	19657	28137	1.17	1.6E-01	AE001862.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3685	16296	28765	1.35	1.6E-01	AJ003165.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
3685	16296	28768	1.35	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
3840	16439	28901	0.71	1.6E-01	AE000962.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
4072	16688		2.65	1.6E-01	AE004413.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4422	17007	29450	11.02	1.6E-01	AF179880.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4554	17137		3.42	1.6E-01	AW868601.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
							EST1380677 MAGE resequences, MAGJ Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4563	17146		4.68	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cc3), mRNA
5057	17630	30074	0.84	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MCLH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
5080	17653	30083	1.45	1.6E-01	AA088343.1	EST_HUMAN	284409.s1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:511381 3' similar to TR:E221865
5101	17673	30112	1.28	1.6E-01	AJ006356.1	NT	E221865 38,865 BP SEGMENT OF CHROMOSOME XIV.;
5101	17673	30113	1.28	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5358	17818		1.81	1.6E-01	BF208302.1	EST_HUMAN	Lycopodium obscurum RsaI fragment 2, satellite region
5359	17919	30333	1.23	1.6E-01	A1874074.1	EST_HUMAN	601872523F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4086895 5'
5587	18218	30688	0.76	1.6E-01	L40608.1	NT	wn48c08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2439182 3'
5713	18339	30844	2.78	1.6E-01	AW197486.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5713	18339	30845	2.78	1.6E-01	AW197486.1	EST_HUMAN	wn43001.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5725	18351	31054	2.12	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;
6178	18789	31558	0.84	1.6E-01	BE925803.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
6559	19157	31953	2	1.6E-01	AL161588.2	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6559	19157	31954	2	1.6E-01	AL161588.2	NT	RC3-BN0034-310800-113-H01 BN0034 Homo sapiens cDNA
7043	18083	30453	3.49	1.6E-01	AW291215.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7753	20261	33157	1.44	1.6E-01	AW248356.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7770	20278		0.75	1.6E-01	AU136825.1	EST_HUMAN	UI-H-B12-egl-b-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7810	20353	33262	1.43	1.6E-01	L48349.1	NT	2822248.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7888	20510		0.55	1.6E-01	BE244087.1	EST_HUMAN	AU136825 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
8062	20604	33515	0.78	1.6E-01	U38243.1	NT	Gorilla gorilla androgen receptor gene, partial exon
8567	21106	34025	0.77	1.6E-01	Z99119.1	NT	TCBAP1E0007 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0807
8760	21298	34220	0.65	1.6E-01	R13673.1	EST_HUMAN	Bacteroides vulgatus beta-lactamase (cbaA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8863	21402		0.64	1.6E-01	L36861.1	NT	Bacillus subtilis complete genome (section 18 of 21): from 2997771 to 3213410
8901	21439	34362	1.91	1.6E-01	Z49501.1	NT	Yf80h08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
9039	21576		0.8	1.6E-01	AF111167.2	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9569	22069		1.93	1.6E-01	BF375171.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJF001w
9572	22072	35033	1.86	1.6E-01	Z49501.1	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene

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9807	22107		1.08	1.0E-01	BE155934.1	EST_HUMAN	PM2-HT0353-270100-004-F11 HT0353 Homo sapiens cDNA
10536	23073	36087	2.7	1.0E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111189-028-G01 CT0220 Homo sapiens cDNA
10880	23401	36418	1.55	1.0E-01	BE258849.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3181183 5'
10894	23508		8.03	1.0E-01	AF100084.1	NT	Pleurokinase calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11289	23741	36798	10.88	1.0E-01	8871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA
11680	25019		1.72	1.0E-01	8879468	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
11784	24169	36776	5.34	1.0E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GCEMF07 5'
12095	24382	30868	1.55	1.0E-01	L14833.1	NT	Rat carboxypeptidase PCS mRNA, 5' end
12126	24382		1.75	1.0E-01	AW839711.1	EST_HUMAN	UCuomis sativus KS mRNA for anti-leucine synthase, complete cds
12228	24821		11.74	1.0E-01	AB045310.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12407	24584		5.11	1.0E-01	AK024468.1	NT	Fuchsiella hybrid cultivar Qiu 84208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12497	24625		3.96	1.0E-01	AF287344.1	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
12521	24637	30896	1.88	1.0E-01	9506522	NT	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
269	12828	25412	1.76	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA
269	12828	25413	1.76	1.5E-01	BE710087.1	EST_HUMAN	AV711688 DCA Homo sapiens cDNA clone DCAADH08 5'
613	15387		2.18	1.5E-01	AV711688.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
815	13433	25038	1.04	1.5E-01	AL163284.2	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1131	13734	26244	0.84	1.5E-01	AJ009735.1	NT	Homo sapiens partial SL C22A2 gene for organic cation transporter (OCT2), exon 1
1136	13739	26248	2.28	1.5E-01	AJ251885.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1152	13756		1.61	1.5E-01	L36125.1	NT	3x39d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1258	13855	26371	0.79	1.5E-01	AW195516.1	EST_HUMAN	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1318	13912	26432	3.12	1.5E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1318	13912	26433	3.12	1.5E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds
1529	14121	26680	1.84	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Meck1) mRNA, complete cds
1851	14535	27091	1.62	1.5E-01	AW444451.1	EST_HUMAN	UH-HB13-ekb-b-09-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2738	15291	27859	1.17	1.5E-01	BF695381.1	EST_HUMAN	602083268F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
							xw56a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_mai
2838	15554		1.01	1.5E-01	AW572516.1	EST_HUMAN	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3070	15885	28157	0.62	1.5E-01	M81441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
							cc88a05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3395	16003	28484	6.87	1.5E-01	AA835048.1	EST_HUMAN	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3415	16023	28504	0.65	1.5E-01	Z23104.1	NT	L stagnalis mRNA for G protein-coupled receptor
3415	16023	28505	0.65	1.5E-01	Z23104.1	NT	L stagnalis mRNA for G protein-coupled receptor

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3474	16080	28553	0.89	1.5E-01	AW612237.1	EST_HUMAN	h25802.x1 NCL_CGAP_JL24 Homo sapiens cDNA clone IMAGE:2658539 3' similar to contains element MER16 repetitive element:
3819	16419	28881	2.13	1.5E-01	U08884.1	NT	Mus musculus ICR/Swiss glyceralddehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3835	16434	28886	0.94	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3849	16447	28908	0.58	1.5E-01	M97882.1	NT	XfNA; Thermosaccharibacterium; xfNA; 4182 base-pairs
3894	16532	28989	2.74	1.5E-01	AW685883.1	EST_HUMAN	H10005.x1 Sacras_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
3951	16549	29017	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3951	16549	29018	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4124	16717	29173	0.82	1.5E-01	AW388859.1	EST_HUMAN	RC2-HT0149-191089-012-c09 HT0149 Homo sapiens cDNA
4282	16848	29296	9.62	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4833	17411	28884	1.29	1.5E-01	BF687885.1	EST_HUMAN	602087192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4863	15291	27659	2.03	1.5E-01	BF685381.1	EST_HUMAN	602083268F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4906	17481	29838	0.82	1.5E-01	BE173798.1	EST_HUMAN	GMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4908	17481	29839	0.92	1.5E-01	BE173798.1	EST_HUMAN	GMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5139	17711	30141	1.59	1.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5481	18098	30414	1.96	1.5E-01	P07896	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5489	18123	30530	0.8	1.5E-01	AF258852.1	NT	Caiman crocodilus MHC class II beta chain (hclibeta) gene, complete cds
5531	18163		5.6	1.5E-01	P15198	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5729	18355	31059	4.68	1.5E-01	AW850764.1	EST_HUMAN	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5767	18383	31106	6.97	1.5E-01	U65016.1	NT	IL3-CT0219-160200-084-F10 CT0219 Homo sapiens cDNA
5767	18383	31107	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
6158	18789	31532	1.4	1.5E-01	6753659	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
6156	18789	31533	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6194	18804	31573	1.98	1.5E-01	AJ276505.1	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6342	18948	31725	3.23	1.5E-01	BE727658.1	EST_HUMAN	Mus musculus genomic fragment, 279 Kb, chromosome 7
6394	18987		1.86	1.5E-01	4506398	NT	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6484	19085	31867	1.75	1.5E-01	AF134907.1	NT	Homo sapiens RAD54 (S. cerevisiae)-like (RAD54L) mRNA
6828	24765	32027	1.94	1.5E-01	AE001039.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6852	18248	32050	4.63	1.5E-01	11417236	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
							Homo sapiens chromosome 5 open reading frame 3 (CSORF3), mRNA

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6863	18259	32063	1.5	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6702	18297	32101	2.16	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6786	18377	32192	0.95	1.5E-01	AA714760.1	EST_HUMAN	nm30410.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6813	18404	32220	1.59	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7055	18074	30484	6.39	1.5E-01	AW070265.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
7268	18786		1.9	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7423	18947	32813	1.5	1.5E-01	AI973157.1	EST_HUMAN	wf52a08.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
7589	20104	32979	1.02	1.5E-01	AF28073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7588	20104	32980	1.02	1.5E-01	AF28073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7596	20110	32984	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-ekk-4-05-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'
7596	20110	32985	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-ekk-4-05-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'
7722	20230	33119	0.71	1.5E-01	U48580.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of <i>ts1-1</i> (SOL3) gene, complete cds
8002	20544	33446	1.1	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK88 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8161	20702	33817	0.95	1.5E-01	AA970317.1	EST_HUMAN	cds5g12.s1 NCI_CGAP_K145 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8254	20785		1.11	1.5E-01	BE884789.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8339	20880		11.5	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8372	20912	33832	1.82	1.5E-01	L27835.1	NT	G16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-529H09 5'
8529	21068	33987	2.04	1.5E-01	D64476.1	NT	Pangasinodon glycos growth hormone (GH) mRNA, complete cds
8550	21089		0.86	1.5E-01	P43449	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8772	21311	34234	1.23	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
8033	21570	34499	2.40	1.5E-01	NT4226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9121	21657	34598	1.08	1.5E-01	BF585465.1	EST_HUMAN	z869a08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:206968 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9128	21683		2.63	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9326	21840		0.94	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAH12 5'
9374	20313	33215	7.21	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9731	22229	35208	0.48	1.5E-01	M77144.1	NT	Acipenser transmontanus vitellogenin mRNA, partial cds
9835	22333	35314	8.51	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
9835	22333	35315	8.61	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10104	22589	35591	2.54	1.5E-01	X08852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10188	22683		3.34	1.5E-01	AB027759.1	NT	P.lentusculus mRNA for integrin beta subunit
							Mesocricetus auratus mRNA for collagen type XVII, complete cds

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10210	22705	35698	2.82	1.5E-01	AI814046.1	EST_HUMAN	wf53h12.x1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10210	22705	35699	2.82	1.5E-01	AI814046.1	EST_HUMAN	wf53h12.x1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10288	22763	35775	1.75	1.5E-01	U40832.1	NT	Danio rerio transcription factor Pax6b (Pax6) mRNA, complete cds
10433	22827	35933	1.97	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10433	22827	35934	1.97	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10704	23233	36245	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10704	23233	36246	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10854	23468	38494	1.71	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11045	18947	32813	2.44	1.5E-01	AI873157.1	EST_HUMAN	wf52c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11739	24875		70.5	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12125	24381		1.43	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12180	24898		7.05	1.5E-01	R63077.1	EST_HUMAN	y887c04.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12288	24920		3.12	1.5E-01	AV741272.1	EST_HUMAN	AV741272 C8 Homo sapiens cDNA clone CBDA004 5'
12408	24824	30794	18.12	1.5E-01	AI138074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/8
12621	24689	30862	3	1.5E-01	Q820Y8	SWISSPROT	VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (CAV1.3)
12832	24708	30865	11.33	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
321	12875		1.48	1.4E-01	AF009883.1	NT	Homo sapiens T cell receptor beta locus, TORBV855P to TORBV21S2A2 region
943	13556		2.71	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1302	13806		1.59	1.4E-01	T81864.1	EST_HUMAN	y454c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1784	14374		1.35	1.4E-01	6876860	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1787	14377	28921	1.39	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
2029	14811		10.08	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2614	15078	27650	1.4	1.4E-01	P30708	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2818	15370	27940	4.1	1.4E-01	AI933498.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U22 Homo sapiens cDNA clone IMAGE:2441865 3'
4253	16841	28280	10.32	1.4E-01	AI690094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4253	16841	28291	10.32	1.4E-01	AI690094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4321	16907	28349	3.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z50b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:X01057_maf1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4501	17085		0.61	1.4E-01	AA776287.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
4784	17384	28815	0.59	1.4E-01	5453861	NT	

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5328	17890		1.74	1.4E-01	BE910013.1	EST_HUMAN	601488056F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900167 5'
5509	18142	30554	4.49	1.4E-01	T80877.1	EST_HUMAN	ye15c11.s1 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:117812 3'
5532	18164	30577	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5532	18164	30578	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6440	18042	31830	2.7	1.4E-01	BE326801.1	EST_HUMAN	h187c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6608	19205	32012	6.4	1.4E-01	AJ1117147.1	EST_HUMAN	AU1117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000789 5'
6608	19205	32013	6.4	1.4E-01	AJ1117147.1	EST_HUMAN	AU1117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000789 5'
6686	19282	32085	3.78	1.4E-01	AW082786.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6686	19285		1.53	1.4E-01	BE266538.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6718	19312	32115	2.07	1.4E-01	BF378533.1	EST_HUMAN	QV1-UW0036-080300-103-008 UM0036 Homo sapiens cDNA
7180	19712		0.81	1.4E-01	AL118588.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7419	18943		1.83	1.4E-01	AW016373.1	EST_HUMAN	UH-BID-eat-c-09-D.U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7617	20130	33005	1.94	1.4E-01	U85845.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphatase (AldB) gene, complete cds
7733	20241	33132	1.77	1.4E-01	AI805192.1	EST_HUMAN	q180b12.x1 Soares_NhiMPu_S1 Homo sapiens cDNA clone IMAGE:1876583 3'
8410	20650		1.28	1.4E-01	AV658047.1	EST_HUMAN	AV658047 GLC Homo sapiens cDNA clone GLCFSH08 3'
8719	21258		0.62	1.4E-01	AI436083.1	EST_HUMAN	h92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 O02710 GAG POLYPEPTIDE.
8844	21383	34308	4.58	1.4E-01	AA307073.1	EST_HUMAN	EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8924	21462	34379	0.62	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9050	21587	34518	1.21	1.4E-01	R82748.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 6'
9050	21587	34519	1.21	1.4E-01	R82748.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9114	21650	34591	8.48	1.4E-01	BF310559.1	EST_HUMAN	601805465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9199	21716	34690	1.09	1.4E-01	W93411.1	EST_HUMAN	z084a04.r1 Soares_Fetal_Heart_Nb1H19W Homo sapiens cDNA clone IMAGE:357102 5' similar to element KER repetitive element;
9280	21806	34757	1.47	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9280	21808	34758	1.47	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9371	20310	33213	1.96	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lal (JAL), and zinc finger protein (DNZ1) genes, complete cds
9698	22395	35371	1.18	1.4E-01	AF023813.1	NT	Macronitrium levatum small ribosomal protein 4 (ps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10000	22495	35484	0.51	1.4E-01	AW021908.1	EST_HUMAN	df28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10000	22495	35485	0.51	1.4E-01	AW021908.1	EST_HUMAN	df28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22652	35645	0.72	1.4E-01	BF375285.1	EST_HUMAN	MF3-ST0218-211288-013-008 S10218 Homo sapiens cDNA
10157	22652	35646	0.72	1.4E-01	BF375285.1	EST_HUMAN	MF3-ST0218-211288-013-008 S10218 Homo sapiens cDNA

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10360	22854		0.73	1.4E-01	T84283.1	EST_HUMAN	y47d03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111365 5'
10489	22983	35991	0.7	1.4E-01	Z06117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2589451 to 2612870
10587	23122		1.89	1.4E-01	AA611480.1	EST_HUMAN	ca9da03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
10722	23250	36265	3.2	1.4E-01	R53400.1	EST_HUMAN	y170c05.r1 Soares breast 2NblHBst Homo sapiens cDNA clone IMAGE:154088 5'
10874	23489	36519	1.66	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11172	23679	36724	1.82	1.4E-01	X66082.1	NT	C-perfringens ORF for putative membrane transport protein
11210	18943		1.96	1.4E-01	AW015373.1	EST_HUMAN	U1H-BID-est-c-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710288 3'
11344	23042	36952	2.4	1.4E-01	U28780.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
12061	24344	30963	4.44	1.4E-01	X74773.1	NT	P. salina plesid gene secY
12074	24352		3.65	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
12123	25082		1.52	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12223	24444		9.33	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transformylase (GAR1) genes, complete cds
12235	24451		1.96	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12315	25098		1.77	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12340	24522		2.01	1.4E-01	AA452305.1	EST_HUMAN	z330e12.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788014 5' similar to contains Alu repetitive element.
12545	24900		3.55	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
12627	24705		1.33	1.4E-01	AW377898.1	EST_HUMAN	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
344	12696	25481	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
344	12698	25482	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
555	13186	25684	3.25	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
684	13268	25769	3.03	1.3E-01	AJ277806.1	NT	Human calicivirus HUJNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/UK
684	13268	25770	3.03	1.3E-01	AJ277806.1	NT	Human calicivirus HUJNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/UK
877	13491	26009	0.78	1.3E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
927	13540	26058	1.44	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1064	13699	26179	1.36	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1168	13768		2.03	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1257	13854	26370	1.36	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1493	14085		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2002	14584	27143	2.32	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2215	14790		1.21	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB8, pucA8, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2329	14900		1.58	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-412 ST0173 Homo sapiens cDNA
2421	14989		3.74	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2622	15184	27750	1.55	1.3E-01	M86918.1	NT	Cerastium auratus keratin type I mRNA, complete cds
3402	16011	28480	0.61	1.3E-01	AF198778.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α)
3498	16103	28578	0.89	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolylacyl transacylase mRNA, complete cds
3785	16385	28850	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3785	16385	28851	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3791	16391	28856	0.8	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodihydroxydehydrogenase 4 [AKR1C4], exon 2
3848	16385	28850	0.82	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3848	16385	28851	0.82	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3875	16473	28937	0.74	1.3E-01	6878940	NT	Rattus norvegicus Fibronectin, gamma polypeptide (Fgg), mRNA
4080	16857		1.3	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4125	13288	25769	1.65	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
4125	13288	25770	1.65	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
4218	16808		0.95	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4238	16828		4.04	1.3E-01	AW304341.1	EST_HUMAN	QV3-DT0018-081289-036-e03 DT0018 Homo sapiens cDNA
4248	16834	28285	2.25	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4265	16851	28299	21.7	1.3E-01	AW273741.1	EST_HUMAN	sv23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4404	16889		1.55	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4577	17160	29603	0.62	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolylacyl transacylase mRNA, complete cds
4631	17214	29665	2.35	1.3E-01	BE272339.1	EST_HUMAN	601128038F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2880063 5'
4698	18009		0.94	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3911987 5'
5056	17629	30073	1.05	1.3E-01	D78842.1	EST_HUMAN	HUM520C02B Human placenta polyA+ (Tfujikura) Homo sapiens cDNA clone GEN-520C02 5'
5279	17841	30288	4.06	1.3E-01	AI432531.1	EST_HUMAN	ff38c10.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
5366	17854	30365	0.65	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1166000 nt. position (5/7)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5444	17869	30402	13.66	1.3E-01	AA981841.1	EST_HUMAN	α45α07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5444	17869	30403	13.66	1.3E-01	AA981841.1	EST_HUMAN	α45α07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5528	18180	30575	0.69	1.3E-01	AW466988.1	EST_HUMAN	hα07α08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 L1 repetitive element;
5565	18196	30642	2.76	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-α08 UMD0093 Homo sapiens cDNA
5682	18318		0.78	1.3E-01	AF107783.1	NT	Emaricella nidulans DNA-dependent RNA polymerase II RP8140 (RP82) gene, partial cds
5772	18397		0.78	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_CL10 genome polypeptide-gene, partial cds
5899	18521	31246	0.89	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6609	18206	32014	15.81	1.3E-01	AB031328.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6884	18280	32083	2.07	1.3E-01	X68891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6883	19818		0.82	1.3E-01	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7305	19833		1.94	1.3E-01	H49684.1	EST_HUMAN	YJ33402.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:207075 5'
7900	20442		0.67	1.3E-01	BE272338.1	EST_HUMAN	601126095F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2690063 5'
7914	20456	33362	1.62	1.3E-01	11423294	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
7945	20487	33397	0.98	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286074 3'
8180	20721		0.47	1.3E-01	BE562528.1	EST_HUMAN	601333829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688634 5'
8286	20827		4.81	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8325	20869		3.78	1.3E-01	8823919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8465	21005	33823	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286074 3'
8878	21416	34338	0.52	1.3E-01	R11172.1	EST_HUMAN	YJ39g11.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN ;
8878	21416		0.52	1.3E-01	R11172.1	EST_HUMAN	YJ39g11.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN ;
8146	21681	34625	1.94	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
8146	21681	34626	1.94	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
8363	21816	34766	5.08	1.3E-01	AF023128.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
9896	22185		0.8	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 2B
9894	22459		0.8	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10036	22531	35526	0.83	1.3E-01	AW851589.1	EST_HUMAN	MR2-CT0222-201089-001-α01 CT0222 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10282	24797	35776	0.9	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10417	22911	35911	0.82	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10511	23049		3.33	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
10975	23460	36520	1.58	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC8A3) gene, complete cds
11130	23638		5.15	1.3E-01	6071745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11468	23918	36984	3.61	1.3E-01	BE279449.1	EST_HUMAN	601159052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11802	24241	31007	1.64	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3686003 5'
12048	24332		3.27	1.3E-01	AJ242790.1	NT	Gallus gallus sox1 gene for lymphoblastin, exons 1-3
12486	24594		1.63	1.3E-01	AW001114.1	EST_HUMAN	wu24009.x1 Soares_Dickgraefe_coton_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to
12847	24721		1.84	1.3E-01	BE958903.1	EST_HUMAN	TR-O60287 O60287 KIAA0539 PROTEIN. ;
406	13061	25573	10.81	1.2E-01	AI421744.1	EST_HUMAN	601644622R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928860 3'
449	13678		1.43	1.2E-01	U68912.1	NT	ANNEXIN V (HUMAN);
573	13203		2.58	1.2E-01	AF039442.1	NT	Dichytalium discoidium ORF DG1016 gene, partial cds
1419	14012	26541	2.31	1.2E-01	AU149148.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1419	14012	26542	2.31	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1428	14019		3.26	1.2E-01	AV735249.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1431	14023		6.69	1.2E-01	AL445066.1	NT	AV735249 cda Homo sapiens cDNA clone cdAAJB11 5'
1554	14146		1.19	1.2E-01	AA897474.1	EST_HUMAN	Thermoplasma acidophilum complete genome; segment 4/5
1673	14285	26709	1.48	1.2E-01	Q14634	SWISSPROT	648609.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TRQ16871
1691	14283	26819	2.77	1.2E-01	AI285402.1	EST_HUMAN	Q16871 ANTH-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1805	14395		21.02	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1984	14548		2.23	1.2E-01	AW448388.1	EST_HUMAN	q68909.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
2228	14801	27373	1.31	1.2E-01	BF248480.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
2325	14898	27470	1.08	1.2E-01	AL163213.2	EST_HUMAN	UI-H-B13-ek-e-10-0-JL.s1 NCI_CGAP_Su65 Homo sapiens cDNA clone IMAGE:2734554 3'
2416	14884		1.05	1.2E-01	Z31405.1	EST_HUMAN	601621657F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2625	15167	27754	1.36	1.2E-01	AW686556.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
				1.05	Z31405.1	EST_HUMAN	HSAAAE8Z1 TEST1, Human adult Testis tissue Homo sapiens cDNA
				1.36	AW686556.1	EST_HUMAN	QV3-BND046-220300-126-f10 BN0048 Homo sapiens cDNA
						EST_HUMAN	1s18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2728988 3' similar to TR.Q14048 Q14048
2754	15309	27675	1.11	1.2E-01	AI623388.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive element ;
2868	15486	27659	1.22	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

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2827	15543	28019	2.37	1.2E-01	A1720470.1	EST_HUMAN	ss80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb1.05095
2861	15577	28056	3.28	1.2E-01	M16384.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3037	15653	28132	0.83	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3267	15678	28362	2.08	1.2E-01	AW370888.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3268	15807		1.19	1.2E-01	U67800.1	NT	QV1-BT0259-281089-021-405 BT0259 Homo sapiens cDNA
3525	16130		0.62	1.2E-01	Z89118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3573	16177	28659	0.82	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3573	16177	28660	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3688	16130		1.08	1.2E-01	Z89118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3833	16432		0.64	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4261	16847	29294	1.98	1.2E-01	Z54255.1	NT	601810788R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053698 3'
4261	16847	29295	1.98	1.2E-01	Z54255.1	NT	P. clarid mRNA; repeat region (ID 2MR17)
4402	16867	29431	0.6	1.2E-01	M15861.1	NT	P. clarid mRNA; repeat region (ID 2MR17)
4830	17408	29862	0.98	1.2E-01	Z48183.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
						NT	L. esculentum mRNA for glycylase-1
4809	17484		2.93	1.2E-01	AF221633.1	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5163	17732	30159	1.06	1.2E-01	BF577357.1	EST_HUMAN	602135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4280185 5'
5275	17836	30262	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5275	17836	30263	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5423	17880		1.99	1.2E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 677
5457	18082	30408	0.71	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.e1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
						NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5503	18137	30547	1.13	1.2E-01	AF223391.1	NT	
5513	18146	30557	2.28	1.2E-01	W33035.1	EST_HUMAN	z008d02.1 Soares parathyroid tumor Nb-HPA Homo sapiens cDNA clone IMAGE:321699 5'
5571	18202	30652	2.3	1.2E-01	Z98268.1	NT	Homo sapiens gene encoding pleckstrin (exons 1-13)
5686	18322	30822	0.89	1.2E-01	Z48234.1	NT	M. domestica Barth. Granny Smith adh mRNA for alcohol dehydrogenase
6347	18662	31731	1.81	1.2E-01	BE620945.1	EST_HUMAN	601483518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6395	18698	31777	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6441	18043	31831	2.38	1.2E-01	AW845275.1	EST_HUMAN	ILD-CT0031-221089-113-e04 CT0031 Homo sapiens cDNA
6502	19102	31887	1.59	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6755	18348	32157	0.88	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156388 5'
7833	20375		1.31	1.2E-01	BE007072.1	EST_HUMAN	PM3-BIN0137-280300-002-109 BN0137 Homo sapiens cDNA

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7903	20445	33351	3.58	1.2E-01	AI913753.1	EST_HUMAN	wc89g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
7950	20492	33401	0.72	1.2E-01	Q02389	SWISSPROT	Q89735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:
8251	20792	33709	0.9	1.2E-01	AI832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8335	20876		9.03	1.2E-01	AW083652.1	EST_HUMAN	et171b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49db07.x1 NCI_CGAP_Esc02 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8355	20895		4.17	1.2E-01	AF083772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8392	20832	33852	0.92	1.2E-01	J03956.1	NT	N crassa vacuolar ATPase 67-Kd subunit (vma-2) gene, complete cds
8392	20832	33853	0.92	1.2E-01	J03956.1	NT	N crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8337	21076		0.83	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 272
8623	21182		2.14	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8657	21186		0.85	1.2E-01	X15181.1	NT	M. musculus DNA fragment of Apolipoprotein B gene
9491	21947	34896	2.66	1.2E-01	X77901.1	NT	S. cerevisiae HXT5 gene
9918	22414	35389	2.65	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
10155	22650	35644	0.48	1.2E-01	AJ718396.1	EST_HUMAN	es59g09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2333056 3'
10798	23290		3.58	1.2E-01	D28184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
10944	23460		3.87	1.2E-01	BE962324.2	EST_HUMAN	601855578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3840283 3'
11026	23540		1.62	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11134	23642	36682	2.87	1.2E-01	AF190463.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
11183	23698	36748	1.67	1.2E-01	R40246.1	EST_HUMAN	yf80cd2.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11382	23834		1.8	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11667	24090		4.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFB12 3'
12029	24319		4.43	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 272
12109	25038	30503	3.9	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12228	24447		1.95	1.2E-01	AF188992.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and synthesis gene, partial cds
12230	13203		17.94	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12345	24528		1.81	1.2E-01	X53981.1	NT	R. norvegicus NF68 gene for 68kDa neurofilament
12440	24577	30915	8.5	1.2E-01	AJ299903.1	EST_HUMAN	gp20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12463	24591		2.19	1.2E-01	L10187.1	NT	Xenopus laevis Integrin alpha 3 subunit mRNA, partial cds
12468	24972		9.71	1.2E-01	O98433	SWISSPROT	CYCLIN T

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12649	16130		1.65	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
590	13220	25698	0.8	1.1E-01	AF591003.1	EST_HUMAN	h18d08.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
643	13268	25743	2.98	1.1E-01	AA568006.1	EST_HUMAN	nm008g11.s1 NC1_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_mel1
1082	13697	26207	1.54	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1124	13727		1.48	1.1E-01	AL161560.2	NT	602123847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1201	15435	26314	3.68	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1292	13687	26411	1.89	1.1E-01	D64004.1	NT	EST3384142 IMAGE: resseques, MAGL Homo sapiens cDNA
1568	14160	26691	2.94	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
2353	14924		3.72	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2578	15401		1.24	1.1E-01	6978678	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
2802	15164		1.06	1.1E-01	AW821908.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2880	15498	27968	1.17	1.1E-01	S82418.1	NT	RCO-ST0378-210100-032-g04 ST0378 Homo sapiens cDNA
3068	15983	28165	0.78	1.1E-01	F03285.1	EST_HUMAN	Interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
3385	15994		1.87	1.1E-01	6753231	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3468	16075	28548	2.27	1.1E-01	BE383186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3489	16104	28579	1.59	1.1E-01	X62135.1	NT	601308678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3827088 5'
3538	16143	28626	0.59	1.1E-01	R68948.1	EST_HUMAN	C.reinhardtii nuclear gene on linkage group XIX
3642	16245	28720	0.8	1.1E-01	Y07695.1	NT	y682g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3763	16364		1.35	1.1E-01	P07394	SWISSPROT	Alu repetitive element;
3771	16372	28837	1.61	1.1E-01	X52708.1	NT	A.immerus gene for transposase
4188	16778	29223	1.61	1.1E-01	AW819412.1	EST_HUMAN	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4188	16778	29224	1.61	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4339	16928		12.27	1.1E-01	AF157088.1	NT	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4374	16961	29407	0.63	1.1E-01	AW802056.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4745	17328	29768	1.11	1.1E-01	S44657.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4858	17533	29875	1.21	1.1E-01	Y07695.1	NT	IL5-UM0070-020500-068-e08 UM0070 Homo sapiens cDNA
5169	16784		0.78	1.1E-01	AF030001.1	NT	Tape-1=Integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
5431	17988	30392	4.82	1.1E-01	AV730569.1	EST_HUMAN	A.immerus gene for transposase
5431	17988	30393	4.82	1.1E-01	AV730569.1	EST_HUMAN	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5435	16245	28720	0.57	1.1E-01	Y07695.1	NT	A. immerus gene for transposase
5850	18474		4.49	1.1E-01	AA747218.1	EST_HUMAN	nc76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5914	18536	31261	1.17	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DGK3) gene, exon 8
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039178F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039178F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4186818 5'
6001	18621	31356	2	1.1E-01	X68951.1	NT	S. pombe sba8 gene encoding protein kinase
6031	18650	31391	5.02	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6171	18787	31555	1.75	1.1E-01	AJ007073.1	NT	Homo sapiens LGMD2B gene
6197	18807	31576	1.8	1.1E-01	BE769152.1	EST_HUMAN	PM3-F10024-130600-004-f12 FT0024 Homo sapiens cDNA
6216	18826	31598	7.81	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280869-011-e01 CT0254 Homo sapiens cDNA
6582	19180	31958	1.38	1.1E-01	AF035748.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6598	19186	32001	0.84	1.1E-01	AI216307.1	EST_HUMAN	qg76806.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6721	19315	32118	3.92	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6805	19396		3.07	1.1E-01	AF032922.1	NT	Homo sapiens syntrophin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6888	19823	32458	2.36	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7238	25119		0.97	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050853 5'
7345	24780	32737	0.92	1.1E-01	AP000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (877)
7542	20062	32835	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7542	20062	32836	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7651	20163	33051	1.85	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7682	20183		0.7	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polypeptide synthase
7683	20194	33082	3.53	1.1E-01	AA788784.1	EST_HUMAN	ah31506.s1 Soares_parathyroid_tumor_NhiHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
7809	20451	33358	1.41	1.1E-01	U67482.1	NT	CHROMOGRANIN A PRECURSOR (HUMAN);
8149	20690	33603	1.6	1.1E-01	AA483574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8149	20690	33604	1.6	1.1E-01	AA483574.1	EST_HUMAN	nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8197	20738	33650	1.18	1.1E-01	X01233.1	NT	nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8235	20776		1.15	1.1E-01	AW817818.1	EST_HUMAN	H. sapiens IL15 gene
8292	20833	33755	1.54	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
8752	21291	34211	8.48	1.1E-01	U02482.1	NT	DKFZp547P194.1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P194 5'
8843	21382	34307	0.87	1.1E-01	A1807474.1	EST_HUMAN	Pedicrococcus acitilactici H. plasmid pSMB74 pediocin Aclt production (pap) gene cluster papA, papB, papC and papD genes, complete cds
							wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8838	21476	34397	0.48	1.1E-01	AF050061.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
8873	21511	34433	2.22	1.1E-01	AA182153.1	EST_HUMAN	z983b12.11 Stratiogene muscle 837208 Homo sapiens cDNA clone IMAGE:827743 5'
8873	21511	34434	2.22	1.1E-01	AA182153.1	EST_HUMAN	z983b12.11 Stratiogene muscle 837209 Homo sapiens cDNA clone IMAGE:827743 5'
8882	21588	34528	0.82	1.1E-01	Y12727.1	NT	P.furiosus partial dph5 gene and erg1 gene
9082	21828	34585	2.28	1.1E-01	T72875.1	EST_HUMAN	y418f03.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:IM81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9119	21655		0.67	1.1E-01	BE883280.1	EST_HUMAN	801438872F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3822048 5'
9343	21857		1.13	1.1E-01	BE142305.1	EST_HUMAN	CM3-HT0142-271088-028-g11 HT0142 Homo sapiens cDNA
9417	21928		2.2	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040800-005-408 GN0027 Homo sapiens cDNA
9824	22322		0.5	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10107	22602		1.03	1.1E-01	R80580.1	EST_HUMAN	y68a09.s1 Soares placenta Nb2f-IP Homo sapiens cDNA clone IMAGE:147084 3'
10240	22735	35727	0.88	1.1E-01	U60529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10554	23080	36104	1.6	1.1E-01	AF245277.1	NT	Dichostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
10894	15663	28155	2.12	1.1E-01	F03265.1	EST_HUMAN	HSCIRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
10892	23325		3.23	1.1E-01	AF168032.1	NT	Carassius auratus actinin beta A precursor, mRNA, complete cds
10823	23442	38483	3.76	1.1E-01	R23708.1	EST_HUMAN	y435f12.11 Soares placenta Nb2f-IP Homo sapiens cDNA clone IMAGE:131768 5' similar to contains Alu repetitive element; contains TAR1 repetitive element ;
10931	23449	38470	1.85	1.1E-01	8881351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA
10947	18587	31288	1.56	1.1E-01	AL110985.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11060	23572	38809	1.74	1.1E-01	X70058.1	NT	MLmusculus cytokine gene
11085	23597	38833	3.35	1.1E-01	Z11810.1	NT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
11085	23597	38834	3.35	1.1E-01	Z11810.1	NT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
11188	23691	38738	2.99	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11884	24231		4.01	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12143	24835		3.29	1.1E-01	BE974588.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850804 3'
12597	24694	30880	1.99	1.1E-01	BF239753.1	EST_HUMAN	601606350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1243	13841		2.35	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1315	13809	28429	1.92	1.0E-01	A985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2466577 3' similar to contains MER7.13
1436	14028	28557	2.23	1.0E-01	AL161504.2	NT	MER7 repetitive element ;
2531	15095	27867	0.97	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3593	16167	28849	1.04	1.0E-01	BF033891.1	EST_HUMAN	UHF-B13-abc-d-07-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738420 3'
3782	16382	28847	0.92	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3858849 5'
3804	16503	28884	1.41	1.0E-01	AF287081.1	NT	601606488F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
							Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3904	16503	28905	1.41	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4027	16625	29097	2.82	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-605 NT0048 Homo sapiens cDNA
4498	17080	29529	1.62	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae AF39, section 91 of 94 of the complete genome
4653	17235		0.97	1.0E-01	AI792349.1	EST_HUMAN	an32a04.y6 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4822	17400	29853	1.8	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4920	17495	29946	0.90	1.0E-01	AA765434.1	EST_HUMAN	ca05H03.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304117 3'
5050	17623	30068	2.12	1.0E-01	AW562344.1	EST_HUMAN	EST384414 IMAGE resequences, MAGB Homo sapiens cDNA
5408	17665	30375	1.06	1.0E-01	AV721471.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBBQE10 5'
5415	17872		0.88	1.0E-01	AV763960.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5524	18150		8.57	1.0E-01	W89490.1	EST_HUMAN	zh62H04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
6040	18659		0.95	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ000065 protein, partial cds
6175	18788	31554	11.01	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6477	18078	31861	0.98	1.0E-01	AA481879.1	EST_HUMAN	z441g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:743062 3'
6489	18090	31873	0.82	1.0E-01	AA406039.1	EST_HUMAN	L1.L3 L1 repetitive element;
7091	19682		1.71	1.0E-01	R23821.1	EST_HUMAN	z467c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu
7717	20225		2.33	1.0E-01	Y12488.1	NT	repetitive element;
7874	20418	33324	0.53	1.0E-01	AA861091.1	EST_HUMAN	y434h08.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu
8107	20648		0.8	1.0E-01	4758365	NT	repetitive element;
8429	20869		0.83	1.0E-01	AW169797.1	EST_HUMAN	M.musculus wtn gene
9113	21649	34590	1.08	1.0E-01	AF102855.2	NT	ak32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb:M34182 CAMP-
9416	21625	34873	0.49	1.0E-01	R44693.1	EST_HUMAN	DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
9426	21835		2.05	1.0E-01	M79729.1	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
9469	21868		2.67	1.0E-01	AE001801.1	NT	x108a01.x1 NCI CGAP_UH4 Homo sapiens cDNA clone IMAGE:2876889 3' similar to gb:X17206 40S
9483	21940	34888	0.71	1.0E-01	W01955.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN);contains TAR1.3 TAR1 repetitive element;
9735	22233	35211	1.67	1.0E-01	BF240154.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synapman mRNA, complete cds
9848	22346	35327	8.17	1.0E-01	AB046799.1	NT	y933h04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34549 3'
9848	22346	35328	8.17	1.0E-01	AB046799.1	NT	Human pro-alpha-1(V) collagen mRNA, complete cds
10048	22543		2.05	1.0E-01	AW957425.1	EST_HUMAN	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
10053	22548	35542	0.61	1.0E-01	T51952.1	EST_HUMAN	z66c10.s1 Soares fetal_hear_NbH19W Homo sapiens cDNA clone IMAGE:327282 3'
							z66c10.s1 Soares fetal_hear_NbH19W Homo sapiens cDNA clone IMAGE:4133487 5'
							601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
							Homo sapiens mRNA for KIAA1579 protein, partial cds
							Homo sapiens mRNA for KIAA1579 protein, partial cds
							EST369815 IMAGE resequences, MAGB Homo sapiens cDNA
							y628a06.s1 Stratagene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:72562 3' similar to
							contains Alu repetitive element

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10234	22728	35720	1.08	1.0E-01	BE782750.1	EST_HUMAN	601594604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939098 5'
10537	23074		2.11	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10910	23428	38448	3.33	1.0E-01	BF242948.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10910	23428	38448	3.33	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11278	23731	36788	5.03	1.0E-01	BE780543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939734 5'
11870	24581		3.49	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12104	24988		1.74	1.0E-01	7862165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12122	24380		1.36	1.0E-01	X00854.1	NT	Drosophila melanogaster fcz gene
12336	24519		2.27	1.0E-01	AA737081.1	EST_HUMAN	ntx11c08.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255780 3'
12413	25031		4.74	1.0E-01	U52891.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12445	24581		2.17	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12485	24623		1.83	1.0E-01	BE158805.1	EST_HUMAN	QV4-H10401-211289-084-g03 HT0401 Homo sapiens cDNA
12511	25001		41.15	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12578	24674		7.73	1.0E-01	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/4
2806	15358	27825	0.83	9.8E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pkc-R11) mRNA, complete cds
2813	15385	27834	1.95	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2813	15385	27835	1.95	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3305	15916	28383	1.86	9.8E-02	AF088810.1	NT	Homo sapiens neuridin III-alpha gene, partial cds
4025	16823	29095	0.64	9.8E-02	AB21637.1	EST_HUMAN	zu45c03.58 Scores ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740832 3'
7049	18088	30459	9.12	9.8E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blebbistatin S deaminase, complete cds
7856	20398	33304	0.65	9.8E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2586528 3' similar to contains Alu repetitive element/contains element MIR MIR repetitive element ;
7856	20398	33305	0.65	9.8E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2586528 3' similar to contains Alu repetitive element/contains element MIR MIR repetitive element ;
9181	21758	34704	1.1	9.8E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
589	13219		1.48	9.8E-02	X56338.1	NT	O. sativa RAmYGc gene for alpha-amylose
3179	15792	28263	4.23	9.8E-02	AF184274.1	NT	Daucus carota leucanthyocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4308	18804	28337	8.69	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4308	18804	28338	8.69	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7495	20018		0.99	9.8E-02	X54193.1	NT	Human HIP1P delta mRNA for protein tyrosine phosphatase delta
9178	21755		1.05	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11334	23032	38041	2.27	9.8E-02	BF037421.1	EST_HUMAN	601460783F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884287 5'
11840	24203		1.46	9.8E-02	8383751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1304	13988	28516	1.24	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1628	14221		1.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2301	14874	27450	2.11	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-085-a04 HT0516 Homo sapiens cDNA
4055	18652		4.76	9.7E-02	Q08795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5548	18180	30594	1.01	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5548	18180	30595	1.01	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6165	18777	31541	1.29	9.7E-02	AW954476.1	EST_HUMAN	EST386546 IMAGE resequences, MAGC Homo sapiens cDNA
7340	19867	32731	3.26	9.7E-02	Z89118.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2897771 to 3213410
7824	20468	33374	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7824	20468	33375	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8783	21322	34246	1.47	9.7E-02	AB93984.1	EST_HUMAN	wx78808.x1 NCI_QGAP_Ox38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:V52851_mart1
11076	23588		2.34	9.7E-02	U69337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); Mus musculus ligatin (Lgtn) mRNA, partial cds
2080	14640	27213	1.33	9.6E-02	AD80721.1	EST_HUMAN	aa47d11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878485 3'
2080	14640	27214	1.33	9.6E-02	AD80721.1	EST_HUMAN	aa47d11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878485 3'
4437	17023	28463	7.64	9.6E-02	Z32686.2	NT	Proteus mirabilis fibrinolytic operon, strain H14320
5142	17713	30144	1.03	9.6E-02	AW968230.1	EST_HUMAN	EST378303 IMAGE resequences, MAGI Homo sapiens cDNA
6254	18863		2.74	9.6E-02	BE910038.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3800165 5'
8317	20858		0.61	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9463	21888	34944	1.34	9.6E-02	AV987888.1	EST_HUMAN	AV987888 GKC Homo sapiens cDNA clone GKCAH02 5'
9786	22284		1.35	9.6E-02	BE984895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5'
9852	22447	35429	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
9852	22447	35430	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35544	1.26	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-S copy)
10055	22550	35545	1.26	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-S copy)
10159	22854	35849	3.43	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
10621	23153	38165	7.28	9.6E-02	Z78702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
11588	24013	37082	1.81	9.6E-02	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745382 3'
12486	24817		1.55	9.6E-02	H14589.1	EST_HUMAN	ym19H03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
4177	16768	28217	2.24	9.5E-02	AW982395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5286	17848	30274	1.12	9.5E-02	U63374.1	NT	Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

Table 4

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12378	24886		16.03	9.3E-02	AW468650.1	EST_HUMAN	hd28h12.1 Sources_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
12589	24933		3.18	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bln1 (BING1), leucine (leucine), RafGOS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr
249	12809	25390	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
249	12809	25391	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
249	12809	25392	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2269	14843		1.58	9.2E-02	RS4158.1	EST_HUMAN	yg98f07.1 Sources infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3213	15825	28302	3.92	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3345	15855	28430	0.88	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.a1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:826138 3'
3646	16249		1.16	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4322	16808		1.42	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4398	16861		0.65	9.2E-02	BE298722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4744	17325	28787	1.44	9.2E-02	X98402.1	NT	G. gallus Mla-CK gene
7861	20463	33402	1.75	9.2E-02	T46920.1	EST_HUMAN	yg98c09.11 Stratagene placenta (4637225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:558009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8117	20658	33567	2.11	9.2E-02	X95258.1	NT	H. vulgare xylose isomerase gene
12856	24930		2.09	9.2E-02	Z22150.1	NT	S. dysgalactiae fbaA gene
448	12877	25134	2.83	9.1E-02	X77865.1	NT	O. cuniculus K12 keratin gene
3733	16334		0.95	9.1E-02	AW372588.1	EST_HUMAN	PM2-BT0349-161289-001-f02 BT0349 Homo sapiens cDNA
4582	17185	28808	1.55	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5905	18527	31253	1.5	9.1E-02	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH1, G88, G8c, G8d, G8e, G8f, BAT5, G5b, GSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7420	19844	32809	11.98	9.1E-02	AW160858.1	EST_HUMAN	au174605.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
7698	20180	33067	0.89	9.1E-02	AF000081.1	NT	Aeropyrum pernix genomic DNA, section 47
7895	20204	33097	0.68	9.1E-02	U38073.1	NT	Mus musculus thymopolein zeta mRNA, complete cds
8855	21394	34317	1.05	9.1E-02	Y14378.1	NT	Homo sapiens gamma adducin gene, exon 9
10325	22819		1.39	9.1E-02	T02884.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
10354	22848	35842	1.52	9.1E-02	S74059.1	NT	Tg618-Cy4 actin (Tritonastes gratilae-see urchins, embryos, Genomic, 5275 nt)
10380	22874	35867	0.73	9.1E-02	Y11187.1	NT	A. thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11656	24083		2.35	9.1E-02	8633494	NT	Bacteriophage Mu, complete genome
11898	25038		1.62	9.1E-02	AA179801.1	EST_HUMAN	zp38h12.s1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P43378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA :

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11978	24289		2.21	9.1E-02	AF052696.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12467	24877		17.53	9.1E-02	AJ281390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
12672	24740		1.6	9.1E-02	AF226888.1	NT	Bombyx mori fibroin heavy chain Fib-H (fib-H) gene, complete cds
774	13393	26893	3.92	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1876	14268	26801	6.34	9.0E-02	BE220482.1	EST_HUMAN	h09g10.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2829	15381	27061	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c085-06 from USA envelope glycoprotein (env) gene, partial cds
2829	15381	27852	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c085-06 from USA envelope glycoprotein (env) gene, partial cds
3380	15889	28488	0.83	9.0E-02	AF279135.1	NT	Dicotyledonum discoidium spore coat structural protein SP05 (cotE) gene, complete cds
4387	16873	29422	0.58	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkey, liver, mRNA, 1474 nt]
4387	16873	29423	0.59	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkey, liver, mRNA, 1474 nt]
4775	17356	28808	1.68	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5401	17859	30370	1.12	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
6146	18780	31519	18.48	9.0E-02	W59037.1	EST_HUMAN	za68a12.r1 Soares_fetal_lung_NhrL19W Homo sapiens cDNA clone IMAGE:297894 5' similar to PIR:S52171 S52171 small G protein - human ;
6830	19410		1.1	9.0E-02	BF062851.1	EST_HUMAN	7h63d03.x1 NC1_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
6864	19598	32428	0.77	9.0E-02	R62805.1	EST_HUMAN	y11508.s1 Soares_placenta_Nhr2HP Homo sapiens cDNA clone IMAGE:138903 3'
12300	24497						Escherichia coli strain E2349/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CseD (cseD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tr (tr), OrfU (orfU), >
1486	14079	28817	2.42	9.0E-02	AF022236.1	NT	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1488	14079	28818	1.46	9.0E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2430	14887	27571	9.68	9.0E-02	BE153572.1	EST_HUMAN	PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4277	16863		1.79	9.0E-02	AF286055.1	NT	Atrichum angustatum AtranFla2 protein (AtranFla2) gene, partial cds
4741	17322	29762	1.91	9.0E-02	AA424887.1	EST_HUMAN	zw03d04.s1 Soares_NhrIMPu_S1 Homo sapiens cDNA clone IMAGE:708199 3'
6014	18634	31370	3.35	9.0E-02	AW452122.1	EST_HUMAN	UIH-B13-alo-f-08-0-UI.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
6014	18634	31371	3.35	9.0E-02	AW452122.1	EST_HUMAN	UIH-B13-alo-f-08-0-UI.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
6028	18845	31387	3.24	9.0E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7244	19773	32630	1.79	9.0E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
7559	20077		2.15	9.0E-02	Z78021.1	NT	H.sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA20F8

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7994	20536	33439	0.99	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8072	20614	33628	0.98	8.9E-02	BF701665.1	EST_HUMAN	60212911F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
8072	20614	33528	0.98	8.9E-02	BF701665.1	EST_HUMAN	60212911F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
8534	21073	33983	4.81	8.9E-02	AA306319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9538	22038	34698	0.83	8.9E-02	AI285827.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element
9538	22038	34699	0.83	8.9E-02	AI285827.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element
9848	22147	35118	0.95	8.9E-02	AA330356.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
11721	24884		2.81	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
11872	24224		4.82	8.9E-02	BF68918.1	EST_HUMAN	602128982F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286180 5'
12044	24330		3.07	8.9E-02	9680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hial1), mRNA
12307	25104		1.57	8.9E-02	U40493.1	NT	Ceratitis capitata mariner transposon transposase gene, complete cds
1416	14009	28538	1.36	8.9E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3971	16569	29038	1.08	8.9E-02	AA289128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4106	16700		4.3	8.9E-02	Q00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII-130) (TAFII130)
4390	16976		0.98	8.9E-02	4580423	NT	Homo sapiens paired box gene 8 (entiridia, keratitis) (PAX8), isoform b, mRNA
8918	21458	34376	1.18	8.9E-02	AA151872.1	EST_HUMAN	2789a05.s1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:588288 3'
10997	23511	36543	3.11	8.9E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535948 5'
10997	23511	36544	3.11	8.9E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535948 5'
11142	23650	36892	10.91	8.9E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
11948	24277	31019	1.73	8.9E-02	Z71591.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
3756	16357	28826	3.9	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xp28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3756	16357	28827	3.9	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xp28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4816	17394	29847	1.42	8.7E-02	AF178838.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5284	17828		1.2	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189408 (section 101 of 148) of the complete genome
5517	18149	30561	5.18	8.7E-02	AA288875.1	EST_HUMAN	z555g08.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701438 3'

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5517	18149	30562	5.18	8.7E-02	AA268875.1	EST_HUMAN	z55g08.s1 NCI_QGAP_GC81 Homo sapiens cDNA clone IMAGE:701438 3'
6831	18580	32421	0.75	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcna1 gene for potassium channel protein, exons 10-14
6831	18580	32422	0.75	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcna1 gene for potassium channel protein, exons 10-14
7803	20346	33910	0.46	8.7E-02	AA284532.1	EST_HUMAN	z20e03.s1 Soares ovary tumor NB-HOT Homo sapiens cDNA clone IMAGE:713692 3'
8452	20692	33910	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8452	20692	33911	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10580	23125		2.71	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11191	23698	36745	1.77	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-Ile and tRNA-Ala genes
11835	24268		2.35	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12142	24388		2.72	8.7E-02	6876057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1285	13889	28412	6.51	8.6E-02	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2286	14880	27435	2.47	8.6E-02	BE408887.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838643 5'
3222	15834	28312	2.42	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3708	16307		4.02	8.6E-02	AF153362.1	NT	Dicystostellium discoideum adenyl cyclase (acrA) gene, complete cds
4584	17197	28610	0.58	8.6E-02	U68178.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
6244	18853	31624	5.78	8.6E-02	J10826.1	NT	Homo sapiens LCN1b gene
6512	19112	31899	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6512	19112	31900	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7581	20096	32974	1.14	8.6E-02	P14618	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7871	20413	33319	1.23	8.6E-02	5730098	NT	Homo sapiens Srf2-related CBP activator protein (SRCAP) mRNA
7871	20413	33320	1.23	8.6E-02	5730098	NT	Homo sapiens Srf2-related CBP activator protein (SRCAP) mRNA
8015	20557	33480	0.76	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
8073	20615		0.65	8.6E-02	U60188.1	NT	Dicystostellium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
8652	22151	35121	1.18	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
8688	22187		1.27	8.6E-02	AW652153.1	EST_HUMAN	H20c08.x1 NCI_QGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
10057	22552	35547	0.74	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds
10824	23345	36360	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10824	23345	36361	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11128	23636	36677	4.74	8.6E-02	BF305808.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11128	23636	36678	4.74	8.6E-02	BF305808.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11315	23013	36022	7.58	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
2440	15007	27578	2.52	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5885	18507		1.91	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6162	18775	31537	5.64	8.5E-02	AF233895.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8542	21081	34002	1.76	8.5E-02	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
9750	22248	35230	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
9750	22248	35231	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10379	22873	35888	0.92	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11035	23549		12.56	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11050	23563	38598	4.42	8.5E-02	AB001582.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12354	24814		5.89	8.5E-02	AJ005588.1	NT	Anthraxinum majus mRNA for MYB-related transcription factor
12358	24847		2.27	8.5E-02	AA362834.1	EST_HUMAN	EST172736 Ovary II Homo sapiens cDNA 5' end
2690	15474	27816	3.71	8.4E-02	W68330.1	EST_HUMAN	z444e11.1 Soares_fetal_heart_NBH19W Homo sapiens cDNA clone IMAGE:343532 5'
5200	17765		1	8.4E-02	X01472.1	NT	Drosophila melanogaster copia-like element 17.6
5369	17829	30343	0.88	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5515	18147	30559	8.48	8.4E-02	BE267153.1	EST_HUMAN	601180438F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534393 5'
6791	19382	32197	1.67	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7972	20514	33421	7.35	8.4E-02	BE085074.1	EST_HUMAN	CM3-B10790-280400-182-005 B10790 Homo sapiens cDNA
8776	21315	34237	1.13	8.4E-02	AF218880.1	NT	Homo sapiens atrial precursor (ATRIN) gene, exon 2
10285	22760	35747	1.61	8.4E-02	A1735184.1	EST_HUMAN	es88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
11858	24217	31042	1.92	8.4E-02	R79408.1	EST_HUMAN	O88312 G08-4.;
2056	14637	27208	2.06	8.3E-02	5835680	NT	y63h12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2056	14637	27209	2.06	8.3E-02	5835680	NT	boddes hexagonus mitochondrion, complete genome
3652	16255	28728	8.98	8.3E-02	P75334	SWISSPROT	boddes hexagonus mitochondrion, complete genome
3680	16281	28748	0.68	8.3E-02	AA36797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3680	16281	28749	0.68	8.3E-02	AA36797.1	EST_HUMAN	th82g08.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5418	17873		1.71	8.3E-02	AW802857.1	EST_HUMAN	th82g08.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6406	19009	31781	0.89	8.3E-02	AB42338.1	EST_HUMAN	QV3-NIN1025-030500-179-e04 NN1025 Homo sapiens cDNA
6504	19104	31869	3.05	8.3E-02	AF052883.1	NT	w078f11.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2461581 3'
7822	20464	33371	3.57	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7855	20497		1.31	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dysophrin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds
8241	20782		4.14	8.3E-02	AA987873.1	EST_HUMAN	cg88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.1f L1 L1
9457	21883	34935	1.55	8.3E-02	AW583503.1	EST_HUMAN	repetitive element; cg81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3' la05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9470	21868		1.84	8.3E-02	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10244	22739		0.56	8.3E-02	AF020409.1	NT	Dicotyledonum discolorum Doca (doca) mRNA, complete cds
11550	23998	37070	1.7	8.3E-02	AA700756.1	EST_HUMAN	z63204.s1 Sources_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435367 3' similar to contains element MER22 repetitive element:
11953	25040		1.36	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3828883 5'
1421	14014		9.32	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1542	14134	26868	1.79	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3109	15724		2.23	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3874	16472		1.88	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4079	16875	28136	1.29	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4371	16958	29400	7.76	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29401	7.76	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29402	7.76	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5240	17804	30225	3.53	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5400	17858	30369	0.9	8.2E-02	AU119830.1	EST_HUMAN	AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1006744 5'
5538	18170	30585	1.62	8.2E-02	BE987030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824523 5'
7092	18693	32502	3.11	8.2E-02	AF308555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8707	21248	34169	2.98	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-405 PT0004 Homo sapiens cDNA
8517	22017	34974	4.88	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
8678	22177	35152	2.2	8.2E-02	BE294318.1	EST_HUMAN	60115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355586 5'
11959	24281	31023	5.69	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AF38, section 73 of 94 of the complete genome
12383	24906		4.6	8.2E-02	AF275386.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5929	18551	31278	1.08	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6516	19116	31808	0.97	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7248	19777		0.72	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7582	20097		1.03	8.1E-02	AI692681.1	EST_HUMAN	w838608.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8281	20822	33741	0.62	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8281	20822	33742	0.62	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8628	22324		1.7	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
11371	23823	36896	1.87	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15405	25143	9.1	8.0E-02	AW854653.1	EST_HUMAN	EST368723 IMAGE resequencing, MAGC Homo sapiens cDNA
971	13582	26095	1.13	8.0E-02	U80315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1736	15449	26889	10.86	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1736	15449	26870	10.86	8.0E-02	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1947	14531	27087	3.32	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-808 BT0347 Homo sapiens cDNA
2413	14981	27556	1.14	8.0E-02	D80915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2413	14981	27557	1.14	8.0E-02	D80915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2509	15073		4.88	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2847	13733	26243	0.87	8.0E-02	M23448.1	NT	Dichyosium discoidum cyclic nucleotide phosphodiesterase gene, complete cds
2925	15541	28016	0.84	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3898	18487	28948	0.59	8.0E-02	AW988118.1	EST_HUMAN	EST378191 MAGE sequences, MAGI Homo sapiens cDNA
4149	16738		0.95	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4890	17465	28920	2.28	8.0E-02	AK34202.1	EST_HUMAN	631g02.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4939	17514		5.81	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
6051	18669	31408	3.07	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7232	18669	31408	1.42	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8089	20811	33524	3.68	8.0E-02	AL114983.1	NT	Bethyis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9311	21825	34773	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, Intron 4
9311	21825	34774	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, Intron 4
10063	22558		0.57	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10671	23203	36216	3.69	8.0E-02	AF217786.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
11993	24302	30868	3.6	8.0E-02	AJ005375.1	NT	Drosophila oreana hunchback region
12595	16738		3.88	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2218	14793	27366	4.15	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
3007	15623	28101	11.7	7.9E-02	AF582028.1	EST_HUMAN	ar88c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173846 3' similar to gb:226878
							60S RIBOSOMAL PROTEIN L38 (HUMAN);
3895	16463	26827	0.82	7.9E-02	AF030894.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG8 (cg8), CG2 (cg2), and CG7 (cg7) genes, complete cds
3917	16515	26878	3	7.9E-02	8681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3917	16515	26879	3	7.9E-02	8681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4834	17509		1.36	7.9E-02	AB008018.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
5390	17948	30360	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
5390	17948	30361	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
6798	18389		1.08	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
7875	20517	33424	3.32	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8941	22436	35412	4.71	7.9E-02	A081644.1	EST_HUMAN	ou33b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
8941	22436	35413	4.71	7.9E-02	A081644.1	EST_HUMAN	CE086111
12478	24613		1.42	7.9E-02	A1781639.1	EST_HUMAN	ou33b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1252	13849	26395	1.36	7.8E-02	A1783275.1	EST_HUMAN	CE086111
1252	13849	26396	1.36	7.8E-02	A1783275.1	EST_HUMAN	cg88b01.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
4812	17487	28943	0.87	7.8E-02	BE836331.1	EST_HUMAN	ou33b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
5247	18412		2.77	7.8E-02	BE250048.1	EST_HUMAN	repetitive element ;
							ou33b02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
							repetitive element ;
							PM3-FN0058-140700-005-609 FN0058 Homo sapiens cDNA
							600843059F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859883 5'
7136	19475	32297	1.34	7.8E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7136	19475	32298	1.34	7.8E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8720	21250	34179	1.46	7.8E-02	BE897847.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8813	21352	34274	0.6	7.8E-02	X78344.1	NT	S.cerevisiae CAT8 gene
8883	21521	34447	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8883	21521	34448	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9283	21883	34828	1.08	7.8E-02	AA468354.1	EST_HUMAN	nc88b06.t1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:771731
9717	22215	35180	0.5	7.8E-02	Z09124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3989281 to 4214814
10544	23081	36094	1.87	7.8E-02	U32323.1	NT	Human Interleukin-11 receptor alpha chain gene, complete cds
12394	24550	30806	1.95	7.8E-02	U72847.1	NT	Homo sapiens envelopin (EVPL) gene, exons 15 through 18
1444	15442	28568	0.91	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3647	18250		2.82	7.7E-02	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5128	17701	30135	0.92	7.7E-02	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
7850	20392	33295	5.56	7.7E-02	AA402949.1	EST_HUMAN	zu33d11.t1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
9748	22247	35228	5.97	7.7E-02	F38080	SWISSPROT	TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;
							PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10037	22532	35527	0.75	7.7E-02	A1318682.1	EST_HUMAN	ts80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:20503359 3' similar to gb:Z26878 60S
10037	22532	35528	0.75	7.7E-02	A1318682.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
10889	23410	36428	4.97	7.7E-02	11422757	NT	ts80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:20503359 3' similar to gb:Z26878 60S
12194	24894		1.81	7.7E-02	11438858	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
3434	18042	28523	3.08	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3455	18062	28537	0.87	7.6E-02	AA286447.1	EST_HUMAN	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3615	18218	28697	0.87	7.6E-02	AJ400877.1	NT	601316428F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
4993	17597		2.04	7.6E-02	AW858844.1	EST_HUMAN	EST112214 Carabellum II Homo sapiens cDNA 5' and similar to protodactherin 43
6247	18856	31627	0.7	7.6E-02	A081275.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6497	19088	31882	0.83	7.6E-02	BE379328.1	EST_HUMAN	RC3-CT0347-110300-014-405 CT0347 Homo sapiens cDNA
9292	21882	34839	1.24	7.6E-02	AJ131016.1	NT	an2502.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689730 3'
9811	22309		1.7	7.6E-02	AL139078.2	NT	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
10120	22615	35605	0.52	7.6E-02	BE78002.1	EST_HUMAN	Homo sapiens SCL gene locus
10251	22746		0.49	7.6E-02	BE959638.2	EST_HUMAN	Campylobacter jejuni NCTC1168 complete genome; segment 5/8
10480	22974	35981	0.72	7.6E-02	X92656.1	NT	RC1-HT0545-020800-017-408 HT0545 Homo sapiens cDNA
10480	22974	35982	0.72	7.6E-02	X92656.1	NT	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3638810 3'
11526	23974	37044	2.58	7.6E-02	AW866845.1	EST_HUMAN	L. esculentum mRNA for those phosphate translocator
817	13435	25940	1.18	7.5E-02		NT	L. esculentum mRNA for those phosphate translocator
817	13435	25941	1.18	7.5E-02		NT	QV3-BN0046-150400-151-404 BN0046 Homo sapiens cDNA
4606	17189	29636	0.57	7.5E-02	AB015061.1	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA
8280	20821	33740	1.15	7.5E-02	A184387.1	EST_HUMAN	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA
8444	20984	33899	1.18	7.5E-02	AU116913.1	EST_HUMAN	Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2
9945	22440		0.5	7.5E-02	BF221730.1	EST_HUMAN	ts80b08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA
10387	22881	35975	0.9	7.5E-02	BF206808.1	EST_HUMAN	ENOLASE (HUMAN);
10481	22975	35983	0.71	7.5E-02	X79460.1	NT	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
503	13135	25623	1.23	7.4E-02	AW838547.1	EST_HUMAN	7c61c05.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
1509	14101		0.97	7.4E-02	AF030027.1	NT	MER27 repetitive element;
							601870203F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
							C.fiml DSM 20113 16S rDNA
							RC5-LT0054-280100-011-H09 LT0054 Homo sapiens cDNA
							Equine herpesvirus 4 strain NS80587, complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2816	15178		1.04	7.4E-02	6755068	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitd1), mRNA
3654	16257	28729	0.84	7.4E-02	AI007885.1	EST_HUMAN	wf43001.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4814	17382	28844	1.33	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4911	17486	28942	2.82	7.4E-02	6878442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5052	17625		1.65	7.4E-02	AE000888.1	NT	Methanobacterium thermoautotrophicum from bases 1076134 to 1086763 (section 82 of 148) of the complete genome
5076	17649	30080	1.67	7.4E-02	6878482	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
5303	17951	30384	0.93	7.4E-02	AI012489.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6821	18218		1.84	7.4E-02	R17477.1	EST_HUMAN	ig14006.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7485	20008	32874	0.88	7.4E-02	AA605132.1	EST_HUMAN	no71d02.e1 NCJ_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
7842	20384	33288	1.23	7.4E-02	BE880112.1	EST_HUMAN	601493369F-1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885284 5'
8438	20878	33853	1.2	7.4E-02	U56089.1	NT	Human periodic tyrosophen protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9083	21629	34566	0.92	7.4E-02	AW62805.1	EST_HUMAN	h867d11.y1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9083	21629	34567	0.92	7.4E-02	AW62805.1	EST_HUMAN	h867d11.y1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9360	20289	33197	0.72	7.4E-02	AI672839.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9360	20289	33198	0.72	7.4E-02	AI672839.1	EST_HUMAN	we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9728	22226	35203	0.85	7.4E-02	U62283.1	NT	we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
11600	24043		1.57	7.4E-02	U89282.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
11912	24250		1.29	7.4E-02	11525803	NT	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
12187	25015		4.44	7.4E-02	AW370431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12351	24531	30826	2.8	7.4E-02	BF035098.1	EST_HUMAN	CMA-HT0243-Q81198-037-411 HT0243 Homo sapiens cDNA
12381	24535	30801	1.37	7.4E-02	AJ223459.2	NT	601453813F-1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3857738 5'
494	13127	25613	1.42	7.3E-02	BE964961.2	EST_HUMAN	Aspergillus nidulans prnD, prnX, prnA genes
494	13127	25614	1.42	7.3E-02	BE964961.2	EST_HUMAN	601658738F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3886209 3'
713	13334	25820	2.89	7.3E-02	AE001788.1	NT	601658738F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3886209 3'
1528	15444	26859	4.47	7.3E-02	AW900281.1	EST_HUMAN	Thermotoga maritima section 101 of 130 of the complete genome
1885	15453		16.16	7.3E-02	AL183302.2	NT	CMM-NN1004-130300-284-908 NN1004 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C102
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3,
							TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3,
3838	18437		0.59	7.3E-02	U66059.1	NT	TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T,
5137	17709		1.11	7.3E-02	U12283.1	NT	TCRBV13S9A1SS>
							Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6680	19178	31978	1.56	7.3E-02	AA779977.1	EST_HUMAN	z224a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:U02428 26S PROTEASE SUBUNIT 4 (HUMAN);
7484	20007	32872	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7484	20007	32873	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8109	20650		1.06	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9137	21672		1.38	7.3E-02	AB011080.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11095	19178	31978	3.07	7.3E-02	AA779977.1	EST_HUMAN	z224a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:U02428 26S PROTEASE SUBUNIT 4 (HUMAN);
125	12784	25279	1.38	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
125	12784	25280	1.38	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
1524	14116	26652	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1524	14116	26653	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2585	15148		2.76	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3854	16552	26021	0.59	7.2E-02	AW28322.1	EST_HUMAN	U14794.1 - 05-Q-UL.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732049 3'
4438	17024	29464	3.65	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251850 5'
5223	17768	30207	0.89	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5491	18125	30533	2.8	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5492	18126	30534	8.6	7.2E-02	P11120	SWISSPROT	CALMODULIN
6265	18873		0.83	7.2E-02	BF217698.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7220	19751	32007	1.27	7.2E-02	BF216088.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7261	19789		1.54	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8128	20669	33578	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8128	20668	33579	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8894	21332		0.5	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9495	21995		0.57	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9529	22028	34988	2.28	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUG01 5'
9674	22173	35149	4.69	7.2E-02	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9628	22328	35307	1.01	7.2E-02	BF125398.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028438 5'
9914	22410	35386	2.73	7.2E-02	AW873187.1	EST_HUMAN	h24411.x1 NCI CGAP_Ad1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q82340 Q82340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10254	22749	35737	2.11	7.2E-02	U82885.2	NT	Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28:TS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10370	22884	35857	5.88	7.2E-02	BE585003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10382	22885		3.22	7.2E-02	BE589214.1	EST_HUMAN	601066194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10782	23315	38324	8.18	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11822	24182	31033	1.54	7.2E-02	AA773696.1	EST_HUMAN	af81a04.f1 Soares_NIH-MIPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
11857	24216		4.88	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
11914	24252		2.01	7.2E-02	AA584465.1	EST_HUMAN	nc05h08.s1 NCL_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1088839 3'
11979	24280		3.59	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
11895	24858		7.52	7.2E-02	AW900962.1	EST_HUMAN	CNA-NN1008-200300-116-c11 NN1008 Homo sapiens cDNA
12514	24633		1.85	7.2E-02	AA401779.1	EST_HUMAN	z57c12.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728454 5'
1848	14532	27088	1.42	7.1E-02	L02280.1	NT	Human Immunodeficiency virus type 1 (D8) proviral structural capsid protein (gag) gene, partial cds
2331	14802	27473	4.53	7.1E-02	BF208602.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082881 5'
7848	20390	33282	0.84	7.1E-02	A1125284.1	EST_HUMAN	q82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736822 3'
11700	24113		6.04	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
554	13185	25663	0.97	7.0E-02	Q07082	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1547	14139		1.43	7.0E-02	X98877.1	NT	M. arbutus Mitc-1 gene
1788	14388	26833	0.94	7.0E-02	AA056843.1	EST_HUMAN	z6804.s1 Strategene colon (#637204) Homo sapiens cDNA clone IMAGE:509599 3'
3004	15680	28153	2.03	7.0E-02	AW138152.1	EST_HUMAN	UH-HB1-acy-c-07-0-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3888	16584	28033	1.71	7.0E-02	AA815438.1	EST_HUMAN	af85a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 80S
4118	16712	28186	1.11	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4219	16807		1.11	7.0E-02	AW782862.1	EST_HUMAN	QV4-BTD407-280100-060-e10 BT0407 Homo sapiens cDNA
4284	16880	28327	1.28	7.0E-02	AF077821.1	NT	CNO-UJM0001-080300-270-e12 UM0001 Homo sapiens cDNA
5003	17838	30079	9.58	7.0E-02	BF381887.1	EST_HUMAN	Caris familiaris inducible ribic acid synthase mRNA, complete cds
5580	18211		0.84	7.0E-02	Y09143.2	NT	601818291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7431	18665	32820	0.88	7.0E-02	AV880285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
9027	21584	34493	1.41	7.0E-02	8828113	NT	AV880285 GK Homo sapiens cDNA clone GKCAED6 5'
9515	22015	34973	1.25	7.0E-02	K02801.1	NT	African swine fever virus, complete genome
8883	22360	35340	0.73	7.0E-02	U27286.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
11251	23781	36837	2.88	7.0E-02	AA724295.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
							af89a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:1.14837
							TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
540	13171	25849	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
540	13171	25850	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1378	13971		1.34	6.9E-02	4507888	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3660	16458	28921	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3660	16458	28922	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucosidase specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
5361	17840	30354	3.59	6.9E-02	AF121254.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
7968	20538		1.13	6.9E-02	U12022.1	NT	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8488	21027	33944	1.1	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8488	21027	33945	1.1	6.9E-02	BE567435.1	EST_HUMAN	Barbaric duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
8048	21585	34516	0.61	6.9E-02	U22987.1	NT	Xlaevis XFD2 mRNA for fork head protein
11853	24213		17.91	6.9E-02	X74315.1	NT	PROTEIN TRANSPORT PROTEIN HOFH HOMOLOG
12031	24321		1.96	6.9E-02	P44821	SWISSPROT	Homo sapiens membrane-bound aminopeptidase P (NPEP2) gene, complete cds
12558	24468		3.68	6.9E-02	AF195653.1	NT	ee30f02.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1928	14511	27095	1.83	6.9E-02	AA496759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1928	14511	27098	1.83	6.9E-02	AA496759.1	EST_HUMAN	ee30f02.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1950	14534	27090	3.99	6.9E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
2023	14605	27170	1.68	6.9E-02	BE263781.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBCSR14) gene, complete cds
4651	17233		0.66	6.9E-02	BE141076.1	EST_HUMAN	601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537708 5'
6980	19478		4.63	6.9E-02	BE061890.1	EST_HUMAN	MRO-HT0068-071099-001-c05 HT0068 Homo sapiens cDNA
7324	19851	32713	8.08	6.9E-02	AL163288.2	NT	RC1-BT0254-080300-017-409 BT0254 Homo sapiens cDNA
8230	20771	33680	5.36	6.9E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C068
8230	20771	33691	5.36	6.9E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 56
11846	25064		2.48	6.9E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome, segment 56
11783	24168		2.42	6.9E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Stratiogene Homo sapiens cDNA clone FB4A8 3' and similar to LINE-1
12380	24547		1.37	6.9E-02	AW975839.1	EST_HUMAN	af67805.81 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
12444	24580		2.87	6.9E-02	6910585	NT	EST387948 MAGe resequences, MAGN Homo sapiens cDNA
12650	25008	30614	1.54	6.9E-02	6978885	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1576	14169		1.51	6.7E-02	AF115536.1	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1838	14522	27078	3.82	6.7E-02	AJ220285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP101 allele, complete cds
							qg78904.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3780	16380	28844	4.61	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (CHOX-A)
4842	17420	28873	3.51	6.7E-02	AP001514.1	NT	Bacillus halodurans genomic DNA, section 8/14
7792	20335	33241	0.63	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7792	20335	33242	0.63	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
6518	22018	34875	0.75	6.7E-02	AW137359.1	EST_HUMAN	UIH-B11-acr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
6518	22018	34876	0.75	6.7E-02	AW137359.1	EST_HUMAN	UIH-B11-acr-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
2225	14800	27372	3	6.6E-02	AJ288241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3510	16115	28584	9.7	6.6E-02	R64308.1	EST_HUMAN	y18b10.s1 Soares placenta N62-IP Homo sapiens cDNA clone IMAGE:138578 3'
3524	16129	28609	3.24	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3524	16129	28610	3.24	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4154	16746	28200	1.83	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5114	17888	30122	11.2	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5114	17888	30123	11.2	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5164	17733	30160	0.57	6.6E-02	AA383244.1	EST_HUMAN	z74807.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:U4270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5164	17733	30161	0.57	6.6E-02	AA383244.1	EST_HUMAN	z74807.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:U4270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6858	19284	32089	4.11	6.6E-02	X08411.1	NT	P. vulgaris mRNA for chalcone synthase
7898	20430	33338	1.58	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8408	20849	33868	0.72	6.6E-02	AF06055.1	NT	Dicotyledon discodermidum darlin (dsar) gene, complete cds
8714	21253		0.49	6.6E-02	O60873	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8852	21391	34312	0.52	6.6E-02	9829198	NT	Human respiratory syncytial virus, complete genome
8852	21391	34313	0.52	6.6E-02	9829198	NT	Human respiratory syncytial virus, complete genome
8802	22359	35338	0.58	6.6E-02	A1468752.1	EST_HUMAN	U97908.r1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:2149488 3'
8858	22494	35483	1.54	6.6E-02	Y07848.1	NT	Homo sapiens EWS, glr22, rrp22 and bam22 genes
10028	22524		0.53	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10842	23363	36378	7.09	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-008-a12 SN0064 Homo sapiens cDNA
12251	24462		2.87	6.6E-02	9837891	NT	Mus musculus DIPB gene (Dipb), mRNA
12585	24678		1.38	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
608	13236	25710	1.65	6.6E-02	BF072639.1	EST_HUMAN	601671046F.1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3854178 5'
1024	13635	26151	2.61	6.6E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1435	14028	26556	3.4	6.6E-02	U47824.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1770	14360	28905	1.42	6.6E-02	AE000764.1	NT	Aquifex acidilocus section 98 of 108 of the complete genome
5349	17808	30324	0.88	6.6E-02	D45898.1	NT	Caenorhabditis elegans DNA for ryenodine receptor, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	18373	31081	1.70	6.5E-02	AA443991.1	EST_HUMAN	z46h12.s1 Soares ovary tumor NkH10T Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M28038
6864	18260	32094	0.89	6.5E-02	BF685340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7051	18070	30461	0.96	6.5E-02	U22861.1	NT	602118687F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276029 5'
6854	22352	35332	0.65	6.5E-02	BE963200.2	EST_HUMAN	Azobacter vinelandii ATCC 8048 negative regulator MucB (mucB) gene, partial cds
6854	22352	35332	0.65	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10363	22857	35848	0.59	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10518	23058	36067	5.86	6.5E-02	AA195648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11688	24091		5.28	6.5E-02	M21498.1	NT	z132g05.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12040	24327		3.84	6.5E-02	AF102883.1	NT	Rabbit microsomal epoxide hydrolase
801	13230	25703	1.74	6.4E-02	X94548.1	NT	Nectria haematococca kinase related protein 2 (KRP2) gene, complete cds
5641	18270	30743	1.21	6.4E-02	A191856.1	EST_HUMAN	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
6261	18669	31639	5.4	6.4E-02	AF052733.1	NT	qe07b01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3
6261	18669	31640	5.4	6.4E-02	AF052733.1	NT	LTR8 repetitive element
6534	19134	31827	0.68	6.4E-02	A872896.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6607	19841	32477	4.7	6.4E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
8278	20819		2.68	6.4E-02	8753323	NT	we73g12.x1 Soares Dieckgrafe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2348790 3'
8569	21138	34052	3.59	6.4E-02	AA093305.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
9055	21582	34522	0.85	6.4E-02	AF150185.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
9506	22008		0.81	6.4E-02	BE834083.1	EST_HUMAN	kt419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9633	22133	35088	1.79	6.4E-02	A8011128.1	NT	AF150185 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
10182	22657	35652	0.68	6.4E-02	AF087150.1	NT	RC1-OT0083-150800-014-g08 OT0083 Homo sapiens cDNA
10182	22657	35653	0.68	6.4E-02	AF087150.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
						NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
						NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
						NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37074	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37075	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11931	24971		4.88	6.4E-02	AF107800.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
11988	24298	30883	2.89	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1791	14361	26828	3.03	6.3E-02	AF106905.1	NT	Mus musculus major histocompatibility locus class III regiona Hsc70t gene, partial cds; snRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3684	16286		2.41	6.3E-02	P37082	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6285	18893	31682	1.1	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_94 Homo sapiens cDNA clone IMAGE:4087489 5'
7291	19819		1.05	6.3E-02	X97889.1	NT	H.sapiens gene encoding La autoantigen
9215	21732	34675	0.96	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominica gene, exons 1-3
9827	22423	35397	2.88	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10172	22687		0.87	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10594	18893	31682	3.9	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087489 5'
4337	16824	26365	3.3	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4431	17017		1.04	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPT1) mRNA, complete cds
4682	17264		6.75	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6899	19624	32459	0.76	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7623	20136	33014	0.78	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8877	25123		0.81	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9267	21783	34742	0.5	6.2E-02	AA778450.1	EST_HUMAN	af20506 s1 Soares, total Testes_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9401	21910	34859	1.05	6.2E-02	6877898	NT	Mus musculus chromal cell derived factor receptor 2 (Sifr2), mRNA
11027	23541	36576	1.74	6.2E-02	AF217490.1	NT	Homo sapiens fragile 160 oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11228	23757	36814	1.89	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
11770	25097		6.34	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12200	24426	30951	3.58	6.2E-02	BF112039.1	EST_HUMAN	783708.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q8Y4S8 Q8Y4S8 HYPOTHETICAL 30.3 KD PROTEIN. [1];
277	12934	25420	4.8	6.1E-02	D18471.1	NT	Human mRNA, Xq terminal portion
4063	16680		2.78	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
4768	17340	28786	1.09	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4768	17340	28787	1.09	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6262	18870		1.42	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8207	20748	33681	3.31	6.1E-02	X99288.1	NT	H.sapiens mRNA for B-HLH DNA binding protein
8595	21134	34048	0.95	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8595	21134	34049	0.95	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10808	23142	36153	6.34	6.1E-02	BE178543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11728	25009		23.38	6.1E-02	X70588.1	NT	S japonicum mRNA for serine-enzyme
12317	24880		1.39	6.1E-02	AI888611.1	EST_HUMAN	U55907.x1 NC1_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2282801 3'
12484	24592		7.98	6.1E-02	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1305	13899	28419	1.01	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 138 of the complete genome
2700	15257	27825	1.15	6.0E-02	AW988848.1	EST_HUMAN	EST380924 IMAGE: ressequences, MAGJ Homo sapiens cDNA
2801	15353		1.58	6.0E-02	AB031288.1	NT	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, rRNA-Gln, rRNA-Phe, rRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2803	12777	25259	1.09	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.t1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
2803	12777	25260	1.09	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.t1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
3266	15878	28380	1.24	6.0E-02	AA372378.1	EST_HUMAN	EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3266	15878	28381	1.24	6.0E-02	AA372378.1	EST_HUMAN	EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3697	16298		1.01	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3876080 3'
5104	17878	30118	0.95	6.0E-02	Z67738.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5595	18225		1.89	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT02633-011199-013-b04 BT0253 Homo sapiens cDNA
6384	18088	31748	1.43	6.0E-02	AB07537.1	EST_HUMAN	W48H05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 L1 repetitive element;
7063	18082	30438	2.73	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7063	18082	30439	2.73	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7239	19768	32624	2.17	6.0E-02	BF382348.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049228 5'
7672	20184	33072	1.94	6.0E-02	AL204275.1	EST_HUMAN	qf58c08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754189 3'
8361	20901		0.57	6.0E-02	11488495	NT	Reclinomonas americana mitochondrion, complete genome
9186	21713	34656	1.12	6.0E-02	AI823167.1	EST_HUMAN	ts78a06.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237982 3'
9186	21713	34657	1.12	6.0E-02	AI823167.1	EST_HUMAN	ts78a06.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237982 3'
9327	21841	34782	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9327	21841	34783	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9819	22317	35288	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
9819	22317	35300	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11214	23717		2.13	6.0E-02	AA128386.1	EST_HUMAN	zp97c08.t1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565168 5' similar to gp-X89181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
11885	24295	30982	1.43	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12394	24554		6.04	6.0E-02	AJ809273.1	EST_HUMAN	Wf88h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR-O60298 O60288 KIAA0551 PROTEIN;

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
260	12910	25393	4.76	5.8E-02	AW834719.1	EST_HUMAN	RC1-DT0001-280100-012-910 DT0001 Homo sapiens cDNA
3012	15828	28107	2.75	5.8E-02	AF180269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4768	17349	29789	0.97	5.8E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4768	17349	29800	0.97	5.8E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4852	17430		0.8	5.8E-02	AF168111.1	NT	Duck parvovirus strain 90-2183 capsid protein (VP3) gene, partial cds
4888	17570	30014	0.86	5.8E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
6873	24774	32374	0.67	5.8E-02	AF145880.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
8552	21091	34011	1.98	5.8E-02	9055249	NT	Mus musculus inositol related hexamer 5 (Drosophila) (In5), mRNA
8372	20311		0.82	5.8E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105894 5'
10884	23198		3.41	5.8E-02	6678870	NT	Mus musculus follistatin-like (Fst), mRNA
10889	23419	38438	2.35	5.8E-02	114333360	NT	Homo sapiens rhoin (LOC51189), mRNA
11429	23880		1.83	5.8E-02	AJ240793.1	NT	Gallus gallus HIKC9 telomere junction
968	13579		5.2	5.8E-02	D80110.1	NT	Thiobacillus ferrooxidans marC, marA genes and URF-1
1700	14293	26828	1	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
2888	15504		0.98	5.8E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3725	16326	28793	1.35	5.8E-02	AE001175.1	NT	Thermotoga maritima section 87 of 138 of the complete genome
4448	17032	29473	5.29	5.8E-02	AW051827.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4448	17032	29474	5.28	5.8E-02	AW051827.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4845	17227	29682	5.04	5.8E-02	AJ247505.1	EST_HUMAN	qh58f01.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to
4845	17227	29683	5.04	5.8E-02	AJ247505.1	EST_HUMAN	qh58f01.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to
4674	17256		1.98	5.8E-02	AF086264.1	NT	gb-M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
5294	17856	30282	0.57	5.8E-02	AF275398.1	NT	gb-M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
5294	17856	30283	0.57	5.8E-02	AF275398.1	NT	alternatively spliced
6088	18685	31428	1.52	5.8E-02	AA190694.1	EST_HUMAN	zp86a11.s1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627068 3'
7670	20182	33068	2.73	5.8E-02	M89150.1	NT	Human polymorphic microsatellite DNA
7670	20182	33070	2.73	5.8E-02	M89150.1	NT	Human polymorphic microsatellite DNA
8601	21140	34054	0.76	5.8E-02	AF163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
11871	24223		2.86	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12177	25085		6.45	5.8E-02	AA604288.1	EST_HUMAN	no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3083	15708	28179	1.13	5.7E-02	AI081844.1	EST_HUMAN	cu83b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3107	15722	28183	1.6	5.7E-02	AF119117.1	NT	CE08811:
3769	16370		0.98	5.7E-02	AF001292.1	NT	Homo sapiens dopamine transporter (SLC8A3) gene, complete cds
3871	16469	28632	2.44	5.7E-02	AW868791.1	EST_HUMAN	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XI (ctt-12) and globin XI (ctt-11) genes, complete cds
4795	17373		1.08	5.7E-02	MF5089.1	NT	EST378865 IMAGE resequences, MAGI Homo sapiens cDNA
5334	17895	30310	0.89	5.7E-02	AJ251973.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
6039	18658		0.9	5.7E-02	AF275948.1	NT	Homo sapiens partial steath-1 gene
8086	20637	33548	1.48	5.7E-02	AJ280060.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
9784	22282	35245	0.65	5.7E-02	6681280	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
11087	23579	30617	4.17	5.7E-02	AI752885.1	EST_HUMAN	Mus musculus ec2 oncogene (Ec2), mRNA
11087	23579	30618	4.17	5.7E-02	AI752885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11227	23738		1.58	5.7E-02	AL163303.2	NT	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
12085	24891		12.98	5.7E-02	D50320.1	NT	Homo sapiens chromosome 21 segment HS21C103
12257	24467		1.71	5.7E-02	AJ271735.1	NT	Pig DNA for SPAL-2, complete cds
12334	24985		3.31	5.7E-02	AF217490.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12483	25074		8.94	5.7E-02	AF261280.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds
12622	24700	30863	1.58	5.7E-02	R48513.1	EST_HUMAN	Pan troglodytes apolipoprotein-E gene, complete cds
1574	14167	26838	1.2	5.6E-02	AF094455.1	NT	y84410.s1 Soares breast 2NtH18t Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element:
4748	17327	28789	1.21	5.6E-02	AB013100.1	NT	Hydrocotyle radundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4806	17384	29834	1.2	5.6E-02	AA280588.1	EST_HUMAN	Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6766	19359	32188	5.98	5.6E-02	AW172708.1	EST_HUMAN	z845c01.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:700418 3'
6871	19548	32372	0.9	5.6E-02	AA868182.1	EST_HUMAN	x02e10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2650050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN:
7205	19736	32588	3.1	5.6E-02	BE008001.1	EST_HUMAN	cd47712.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element:
8737	21276	34188	2.2	5.6E-02	BE542883.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
8737	21276	34189	2.2	5.6E-02	BE542883.1	EST_HUMAN	601087159F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8737	21276	34189	2.2	5.6E-02	BE542883.1	EST_HUMAN	601087159F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9728	22224	35201	1.07	5.6E-02	AA482864.1	EST_HUMAN	nt40407.s1 NCL_CGAP_Av1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G768959 G768959
11439	23889		2.33	5.6E-02	AF260225.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 1C.;
2879	15237	27804	6.14	5.5E-02	X97869.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3251	15863	28345	3.83	5.6E-02	6755501	NT	H. sapiens gene encoding La autoantigen
4296	16882	28328	1.12	5.5E-02	L41591.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
5940	18464	31188	3.19	5.5E-02	Q01174	SWISSPROT	Galid herpesvirus mRNA fragment
6176	18484	31188	3.86	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7412	19837	32802	1.77	5.5E-02	6755902	NT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
8063	20605	33516	0.77	5.5E-02	AF170911.1	NT	Mus musculus tufalin 1 (Tuf1), mRNA
8063	20605	33517	0.77	5.6E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8573	22073	35034	0.61	5.5E-02	10947034	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9573	22073	35035	0.61	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9864	22163	35136	1.26	5.6E-02	U69492.1	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
							Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
10898	23418	36435	11.52	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB);>
3054	15670		0.85	5.4E-02	AJ277488.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3489	18013		6.27	5.4E-02	BE073488.1	EST_HUMAN	RC5-BT0559-140200-012-Q03 BT0559 Homo sapiens cDNA
3992	16580	29051	0.58	5.4E-02	U85808.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
5119	17691	30129	2.48	5.4E-02	U53528.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
8067	20609		1.11	5.4E-02	Z89116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395281 to 2813730
9001	21538	34467	0.61	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10578	23113	36126	1.89	5.4E-02	U20790.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11058	23570	36606	1.56	5.4E-02	BF371288.1	EST_HUMAN	RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA
11058	23570	36607	1.56	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA
11968	24882		2.9	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1091	13698	26205	1.58	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-062-ab9 ST0213 Homo sapiens cDNA
1091	13698	26206	1.58	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-062-ab9 ST0213 Homo sapiens cDNA
							ye37112.1 Stragelone lung (#637210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01506
1553	14145	28679	21.83	5.3E-02	T94759.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2541	15105	27877	2.71	5.3E-02	AJ276408.1	NT	Pseudomonas putida tlgS gene
2969	15585	28068	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2969	15595	28067	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3187	15799	28271	4.52	5.3E-02	AJ276408.1	NT	Pseudomonas putida tlgS gene
5248	17811	30234	0.75	5.3E-02	AB051897.1	NT	Mus musculus Scya6, Scya8, Scya10-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya10 pseudogene, small inducible cytokine A5 precursor, complete cds
5250	17813	30236	8.25	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5522	18154	30568	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
5522	18154	30569	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6251	18880	31632	0.71	5.3E-02	M85288.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
6894	19541	32363	4.23	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7149	19882	32523	1.55	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7396	19821		2.05	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
7818	20290	33189	0.52	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8344	20885		0.54	6.3E-02	U10098.1	NT	Mus musculus 128Sv cystatin C (csc3) gene, complete cds
9053	21590	34521	1.83	5.3E-02	X03127.1	NT	Potapora anserina mitochondrial epsilon-sen DNA
10038	22533	35529	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7)-methyltransferase, complete cds
10038	22533	35530	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7)-methyltransferase, complete cds
10156	22651		0.82	5.3E-02	Y07807.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurons, 9-16 hpf and postmitogenesis, 20-28 hpf)
10235	22730	36721	0.65	5.3E-02	X68432.1	NT	B. rerio pou3f1 mRNA for transcription factor
2324	14895		110.52	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3148	15762	28228	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3148	15762	28229	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4013	16011	29084	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4365	16952	29392	3.61	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nar-1 mRNA, complete cds
4846	17424	29877	1.29	5.2E-02	L33246.1	NT	Drosophila melanogaster filament protein homolog (sepi) gene, complete cds
6076	18893	31439	0.89	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6255	18864		1.42	5.2E-02	AJ830665.1	EST_HUMAN	w80604.x1 NC1_CGAP_Lym12 Homo sapiens cDNA clone IMAGE-2408150 3' similar to contains MER15.b1 MER15 repetitive element
7318	19845	32706	1.19	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8136	20677		1.98	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9645	22145	35113	1.97	5.2E-02	D10827.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9645	22145	35114	1.97	5.2E-02	D10827.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12224	24445		1.84	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
12327	24513		1.27	5.2E-02	D68362.1	NT	Mouse DNA for regilla gamma protein, complete cds
2402	14970		1.14	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D073 5'
4282	16888	28315	0.73	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4808	17483	28941	8.03	5.1E-02	AF085167.1	NT	Hordeum vulgare receptor-like kinase ARK1AS gene, partial cds
5205	17770	30193	1.14	5.1E-02	BE957423.2	EST_HUMAN	801653566R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
6777	19389	32182	0.76	5.1E-02	AF280388.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
6842	18050	30472	1.6	6.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8195	20736	33646	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8195	20736	33646	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8288	20828	33750	1.48	5.1E-02	AJ131988.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8818	21357	34282	0.63	5.1E-02	P02533	SWISSPROT	Spodoptera littoralis mRNA for 3-dehydrocyclohexa-beta-reductase
8818	21357	34283	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9723	22221	35198	8.16	5.1E-02	AF012888.1	NT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10084	22579	35572	1.83	5.1E-02	P40603	SWISSPROT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10709	23237	38250	2.86	5.1E-02	AF083930.1	NT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10709	23237	38251	2.86	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12332	24448		1.51	5.1E-02	AF062467.1	NT	Homo sapiens ES18 mRNA, partial cds
508	13141	25828	1.78	5.0E-02	AF088004.1	NT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds
1246	13843	26360	6.63	5.0E-02	Z99104.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
							Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
2034	14616	27182	3.63	5.0E-02	P02810	SWISSPROT	4) (PIF-F/PIF-S) (PROTEIN APROTEIN C) (CONTAINS: PEPTIDE P-C)
2846	13634	28150	1.78	5.0E-02	U72742.1	NT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-3)
3381	15880		1.42	5.0E-02	7305810	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3655	16258		1.08	5.0E-02	U32782.1	NT	Mus musculus Ubc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3747	16348	28816	5.6	5.0E-02	U12769.2	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
5102	17674	30114	1.11	5.0E-02	AF188530.1	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
6279	18887	31856	0.74	5.0E-02	AF086284.1	NT	Homo sapiens ubiquitous tetrahydrocortisol containing protein RoXaN mRNA, partial cds
6450	19051		1.23	5.0E-02	AJ242823.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7544	20064	32838	10.74	5.0E-02	P35616	SWISSPROT	Mus musculus Dmp-1 gene, exons 1-6
10101	22586	35588	1.13	5.0E-02	AF305238.1	NT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
11384	23816	36877	2.87	5.0E-02	AF07600.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fisd3) mRNA, complete cds
11756	24924		7.22	5.0E-02	Q04047	SWISSPROT	Methanococcus jenningsii section 142 of 150 of the complete genome
242	12901		23.23	4.9E-02	M14230.1	NT	NO-ON-TRANSIENT A PROTEIN
							Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	13038	25528	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
392	13038	25528	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3328	15938	28414	1.58	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3628	16231		0.83	4.9E-02	AA189940.1	EST_HUMAN	z48a12.s1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:832828 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3651	16254	28726	0.91	4.9E-02	AA400814.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3651	16254	28727	0.91	4.9E-02	AA400814.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4988	17540	28982	1.59	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2832388 3'
4988	17540	28983	1.59	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2832388 3'
5372	17831	30345	0.81	4.9E-02	7682816	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5408	17884		0.91	4.9E-02	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
5425	17882		0.89	4.9E-02	AE001774.1	NT	Thermoplasma maritima section 88 of 136 of the complete genome
5437	17882	30398	1.03	4.9E-02	M84083.1	NT	Brucella ovis heat shock protein hsp70 (dnaK) gene, complete cds; heat shock protein hsp40 (dnaJ) gene, complete cds
5573	18204	30654	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5573	18204	30655	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7188	19727	32578	0.89	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8551	21080		0.88	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8698	21228	34149	0.7	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10183	22688	35681	0.54	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11280	23733	36788	3.87	4.9E-02	AF083303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12148	24391		1.44	4.9E-02	8823980	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12431	24573		2.92	4.9E-02	M18364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
352	13002	25487	1.15	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
353	13002	26487	1.87	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
514	13147	25631	9.43	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2312	14884	27459	1.98	4.8E-02	W51983.1	EST_HUMAN	z48a02.s1 Soares_senescent_fibroblasts_NHTSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30838 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3244	15856	28338	2.34	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3I and histone H4II intergenic DNA
4778	17358		1.32	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle myosin receptor
5309	17871	30293	0.67	4.8E-02	U91814.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
5380	17939	30352	4.1	4.8E-02	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
5380	17939	30353	4.1	4.8E-02	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8080	20822	33535	1.42	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-Z21088-012-b02 ST0129 Homo sapiens cDNA
9057	21594	34524	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9057	21594	34525	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12018	24315		1.93	4.8E-02	9832893	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
8918	19577	32408	2.98	4.7E-02	W01153.1	EST_HUMAN	yeast709.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Abu repetitive element
8985	19542	32384	0.78	4.7E-02	BF68825.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
8985	19542	32385	0.78	4.7E-02	BF68825.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
8908	19496	32317	1.57	4.7E-02	M82752.1	NT	Rat elastin-related protein (el) gene, complete CDS
8183	20734	33844	8.55	4.7E-02	X15543.1	NT	B. tauren mRNA for RF-38-DNA-binding protein
8883	21421	34348	1.12	4.7E-02	X88211.1	NT	H. sapiens DNA for endogenous retroviral like element
8908	21444		2.28	4.7E-02	A8028678.1	NT	Gallus gallus Wpka-8 gene, complete cds
8154	21689	34633	6.91	4.7E-02	X15543.1	NT	B. tauren mRNA for RF-38-DNA-binding protein
8965	22065	35024	0.55	4.7E-02	BF308237.1	EST_HUMAN	601892882F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
8950	22149		0.55	4.7E-02	A873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10634	23196	36177	1.55	4.7E-02	8754565	NT	Mus musculus ligand of numb-protein X (Lrx), mRNA
11430	23881	36945	1.69	4.7E-02	U73821.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11430	23881	36946	1.69	4.7E-02	U73821.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11951	25087		8.94	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLC8K002 3'
12322	25089		1.47	4.7E-02	P52951	SWISSPROT	HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)
282	12948	25435	0.81	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
769	13388	25887	2.44	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1685 section 335 of 400 of the complete genome
13315	13928		1.37	4.6E-02	A014255.1	EST_HUMAN	sm50402.at Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TRP06053
1403	13906	26525	9	4.6E-02	AV727059.1	EST_HUMAN	P00533 LIMA : contains element LTR1 repetitive element ; AV727059 HTC Homo sapiens cDNA clone HTCBW001 5'
2530	15094	27686	2.77	4.6E-02	AW236023.1	EST_HUMAN	Q12848 G-RICH SEQUENCE FACTOR-1 ; PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
2834	12948	25435	1.83	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
3042	15658	28138	0.7	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
3543	15658	28138	0.95	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
4201	16790		0.97	4.6E-02	AF220365.1	NT	Mus musculus nuclear RNA helicase I/Gu (dtd21) gene, complete cds
5809	18531	31256	1.44	4.6E-02	AF076962.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Grnh2) gene, complete cds
6377	18081	31760	3.77	4.6E-02	X81624.1	NT	C.reinhardtii atp2 (atp8) mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6377	18981	31781	3.77	4.9E-02	X61624.1	NT	C. reinhardtii atp2 (atp8) mRNA
6891	19825	32481	1.39	4.9E-02	A1149574.1	EST_HUMAN	q60b06.x1 Soares_placenta_86c6weeks_2Nbr-IP-80b3W Homo sapiens cDNA clone IMAGE:1713971 3'
8560	21129	34048	2.82	4.9E-02	BE154008.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
11281	23734	36789	4.26	4.9E-02	AA913328.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
12541	24651		2.54	4.9E-02	X57608.1	NT	q27n08.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
472	13105	25598	2.71	4.5E-02	P22448	SWISSPROT	Human germline immunoglobulin lambda light chain gene
1260	13857	28373	0.78	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1280	13857	26374	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain MIS.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1840	14428	26880	3.54	4.5E-02	P32182	SWISSPROT	Marburg virus strain MIS.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
2150	14733	27309	3.85	4.5E-02	AE003984.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3786	16386	28852	3.84	4.5E-02	AL163278.2	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
6378	18982	31782	1.88	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C078
6631	19227	32032	0.89	4.5E-02	AL163280.2	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8332	20873	33785	1.8	4.5E-02	AF036984.1	NT	Homo sapiens chromosome 21 segment HS21C080
9880	22357	35337	5.91	4.5E-02	AA325216.1	EST_HUMAN	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10117	22612	35602	0.77	4.5E-02	AB000470.1	NT	EST28167 Cerebellum II Homo sapiens cDNA 5' and similar to neuro-D4 protein
11947	24276	31018	2.92	4.5E-02	11418013	NT	Gallus gallus mRNA for alpha1 Integrin, complete cds
12367	24973	30638	6.27	4.5E-02	AA191087.1	EST_HUMAN	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
237	12897		3.08	4.4E-02	BE972733.1	SWISSPROT	zq49f1.r1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:832483 5'
2144	14722		0.8	4.4E-02	P31568	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2532	15098	27688	2.82	4.4E-02	AW875475.1	EST_HUMAN	HYPOTHETICAL PROTEIN (ORF 2280)
3702	16303	28771	1.5	4.4E-02	AF159160.1	NT	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
4733	17314	29758	1.23	4.4E-02	AF109907.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4733	17314	29757	1.23	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32551	1.56	4.4E-02	AF085824.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32552	1.56	4.4E-02	AF085824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8687	21226	34146	2.04	4.4E-02	AA738968.1	EST_HUMAN	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
10951	23486	36489	4.58	4.4E-02	AF086688.1	NT	nm13h03.s1 NC1 CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11080	23592	36628	2.63	4.4E-02	AA468739.1	EST_HUMAN	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
							es33104.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:887631 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11884	24088		3.28	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1483 protein, partial cds
813	13431	25836	8.91	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2803	15185	27732	1.16	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0408 5'
3477	16083	28557	8.12	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3720	16321		1.12	4.3E-02	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6822	19219	32023	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6822	19219	32024	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6830	19420	32236	0.68	4.3E-02	AA652268.1	EST_HUMAN	ns68c12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188886
8450	20880	33808	0.74	4.3E-02	AF283359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8738	21276	34198	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8738	21275	34197	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
855	13471	25882	1.57	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
889	13513		2.24	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
929	13542	28080	0.69	4.2E-02	AW003645.1	EST_HUMAN	w034g01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1758	14348		1.32	4.2E-02	AL445066.1	NT	L1 RETROPOSIN, ORF2 mRNA ; contains L1.13 L1 L1 repetitive element ;
							Thermoplasma acidophilum complete genome, segment 4/5
							q05f10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718
3180	15802	28274	0.98	4.2E-02	AI469472.1	EST_HUMAN	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN);
3726	16327	28794	1.36	4.2E-02	P23081	SWISSPROT	TRANSFORMING PROTEIN MAF
4410	16885	28437	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4410	16885	28438	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4854	17432	28883	0.69	4.2E-02	BF342865.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5902	18427	31145	1.49	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5802	18427	31146	1.49	4.2E-02	AF280107.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7534	20054	32827	5.29	4.2E-02	AF276752.1	NT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
8745	21284	34206	3.5	4.2E-02	P05095	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
10069	22564	35559	1.17	4.2E-02	Q16850	SWISSPROT	cn33b11.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65280
10919	23438	36459	3.12	4.2E-02	AA976118.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11187	23692	36739	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-008-d10 BN0174 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11187	23692	36740	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11378	23631	36894	2.06	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12226	25023		3.4	4.2E-02	A1983494.1	EST_HUMAN	w48g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
536	13187	25648	0.7	4.1E-02	AF200626.1	NT	Homo sapiens HPS1 gene, intron 5
2701	15258	27826	2.87	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4571	17154		8.95	4.1E-02	AW883484.1	EST_HUMAN	QV1-NN0012-180400-164-068 NN0012 Homo sapiens cDNA
5285	17857		0.69	4.1E-02	X85880.1	NT	Limonocycogenes type 3 partial lap gene (strain 443)
5824	18448	31170	0.98	4.1E-02	BE261894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5824	18448	31171	0.98	4.1E-02	BE261894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6962	19539		0.97	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7156	19688	32532	1.92	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7522	20042	32911	1.76	4.1E-02	7682347	NT	Homo sapiens KIAA0887 protein (KIAA0887), mRNA
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit?
7742	20250	33143	3.14	4.1E-02	AF026168.1	NT	CUTICLE COLLAGEN 34
8577	21118	34036	0.56	4.1E-02	P34687	SWISSPROT	EST84291 Coton adenocarcinoma IV Homo sapiens cDNA 5' end
9081	21617	34552	0.85	4.1E-02	AA373388.1	EST_HUMAN	Brassica napus gin gene for plastid glutamine synthetase, exons 1-12
12572	25024	30618	24.9	4.1E-02	AJ271609.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3281	19882	28371	3.71	4.0E-02	AB040904.1	NT	Homo retinoblastoma susceptibility gene exons 1-27, complete cds
3668	18468	28829	0.96	4.0E-02	L11910.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
5298	17858	30284	0.58	4.0E-02	AB042287.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5581	18212	30661	5.51	4.0E-02	AF280107.1	NT	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75298 O75298
6362	18868	31744	1.66	4.0E-02	BF110434.1	EST_HUMAN	R29124_1.;
							Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7678	20189	33078	6.8	4.0E-02	L23838.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33144	0.87	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33145	0.87	4.0E-02	AB000381.1	NT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8651	21180	34108	2.64	4.0E-02	P08840	SWISSPROT	GLUCOHYDROLASE
9562	22062		0.84	4.0E-02	BF078376.1	EST_HUMAN	602150884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9586	22086	35051	3.35	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiothymate reductase subunit A

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9895	22392		1.28	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11608	24051		1.62	4.0E-02	AJ001018.1	NT	Karyeromyces laticis gene for Cat+ ATPase
11841	24834	30798	18.69	4.0E-02	AJ001058.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1159	13762	28273	3.8	3.9E-02	BF516149.1	EST_HUMAN	UI-HBW1-ant-h-08-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1390	13984	26510	1.88	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2004	14588	27145	2.67	3.9E-02	AJ403398.1	NT	Mus musculus DNA for desmin-binding fragment DesD7
2728	15283		1.85	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5325	17887	30303	0.6	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5344	17805	30320	1.14	3.9E-02	8824019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5344	17805	30321	1.14	3.9E-02	8824019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5687	18313	30810	0.73	3.9E-02	D50608.1	NT	Rat gene for cholesteryltransferin type-A receptor (CCKAR), complete cds
5687	18313	30811	0.73	3.9E-02	D50608.1	NT	Rat gene for cholesteryltransferin type-A receptor (CCKAR), complete cds
5906	18528	31254	1.24	3.9E-02	BE96841.1	EST_HUMAN	601648874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833842 5'
6018	18637	31377	0.68	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7118	19458	32273	1.01	3.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3046930 5'
7781	20324	33228	0.93	3.9E-02	BF238613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8004	20546	33449	0.56	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
8004	20546	33450	0.56	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
11287	20289	33188	1.6	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11891	24981		7.19	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12373	24543		1.73	3.9E-02	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY3, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
12503	24902		64.84	3.9E-02	AL049896.2	NT	Mus musculus chromosome X contigB: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmoq28orf
1985	14577	27137	1.24	3.8E-02	BE865137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
4987	17571	30015	0.99	3.8E-02	BE863275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628757 5'
4987	17571	30016	0.99	3.8E-02	BE863275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628757 5'
5062	17835	30078	0.93	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5632	18261	30733	1.19	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6237	18846	31617	1.07	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOXB4 (HOX-2.6)
7359	18885	32748	1.43	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8598	21137		1.3	3.8E-02	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
10506	23000		0.47	3.8E-02	AE001329.1	NT	Chlamydia trachomatis section 58 of 87 of the complete genome
10532	23059	36082	2.17	3.8E-02	AF143852.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1029	13639	28154	3.69	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1432	14025	26553	1.15	3.7E-02	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2278	14852	27430	4.48	3.7E-02	AB94806.1	EST_HUMAN	wr5c08.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2613	15175	27743	0.93	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3086	15701	28174	0.97	3.7E-02	P78944	SWISSPROT	ECMESODERMIN
3088	15703	28175	4.74	3.7E-02	BF312863.1	EST_HUMAN	601868233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125594 5'
7138	25118		0.73	3.7E-02	AP000003.1	NT	Aeropyrum pernix genomic DNA, section 67
9828	22424		0.89	3.7E-02	AA782518.1	EST_HUMAN	af55cd0.s1 Soares_parathyroid_tumor_Nbr-IPA Homo sapiens cDNA clone 1360812 3'
11735	24139	37158	7.89	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12435	24886	30707	3.02	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3715	16316	28784	0.82	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3723	16324	28791	0.87	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q28.3] of Homo sapiens
5620	18249	30701	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5620	18249	30717	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
6808	18399	32213	5.32	3.6E-02	AW845516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6808	18399	32214	5.32	3.6E-02	AW845516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7143	19376	32516	1.68	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cyt2 precursor (sgp2) gene, complete cds
7347	19873	32739	3.52	3.6E-02	AA714521.1	EST_HUMAN	rw20e05.s1 NCJ_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_mae2
7629	20141	33020	0.88	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9313	21827	34776	1.87	3.6E-02	U20608.1	NT	MRO-HT0158-030200-003-b08 HTD158 Homo sapiens cDNA
9313	21827	34777	1.87	3.6E-02	U20608.1	NT	Dicystostellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9530	22030	34889	0.72	3.6E-02	BF347568.1	EST_HUMAN	Dicystostellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
928	13541	26059	1.57	3.5E-02	U06506.1	NT	602020453F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156116 5'
1046	13654	26168	2.29	3.5E-02	AF263417.1	NT	Drosophila melanogaster tlggrin mRNA, complete cds
						NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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1610	14203	26736	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1610	14203	26737	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4283	16879	28328	1.91	3.5E-02	AE001773.1	NT	Thermococcus maritima section 85 of 136 of the complete genome
4406	16691	28435	1.16	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6370	18974	31752	2.11	3.5E-02	J01238.1	NT	Maize eth1 gene (MAC1), complete cds
7918	20460		0.82	3.5E-02	H28951.1	EST_HUMAN	yp44a05.11 Soares retina N2551R Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Abu
8558	21097	34018	3.5	3.5E-02	BE958970.1	EST_HUMAN	repetitive element
8631	22427	35401	2.44	3.5E-02	X78642.1	NT	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3629737 3'
8677	22472	35455	0.49	3.5E-02	BE661042.1	EST_HUMAN	Lactis M91303 grpE and dnaK genes
11367	23819	36880	1.92	3.5E-02	AW861641.1	EST_HUMAN	601344681F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11367	23819	36881	1.92	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291298-002-H03 CT0328 Homo sapiens cDNA
12357	24534		1.39	3.5E-02	AF008663.1	NT	PM1-CT0328-291298-002-H03 CT0328 Homo sapiens cDNA
12429	24913		4.38	3.5E-02	BE276948.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV/BS5P to TCRBV21S2A2 region
604	13233	25706	1.18	3.4E-02	AK024424.1	NT	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
604	13233	25707	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25706	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25707	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1089	13694	26203	3.22	3.4E-02	AW274020.1	EST_HUMAN	SV: C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR;
1248	13845		6.54	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2435	15002	27574	1.92	3.4E-02	T57180.1	EST_HUMAN	Homo sapiens lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains
3478	16084	28558	1.11	3.4E-02	AL163208.2	NT	MER29 repetitive element
3843	16442	28903	0.88	3.4E-02	BE839514.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3893	16591	29063	4.29	3.4E-02	AW784952.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4703	17285	28730	3.17	3.4E-02	X59789.1	NT	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
5217	17782		2.61	3.4E-02	Q28457	SWISSPROT	M.musculus S-antigen gene promoter region
5237	17801	30220	1.47	3.4E-02	AJ012489.1	NT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6353	18558		0.89	3.4E-02	BF131628.1	EST_HUMAN	Casarioabditis elegans mRNA for DYS-1 protein, partial
6938	18046	30468	4.83	3.4E-02	U24393.1	NT	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
8204	20745		3.76	3.4E-02	A1868329.1	EST_HUMAN	Human lysyl oxidase-like protein gene, exon 3

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8682	21221	34141	1.84	3.4E-02	AA684886.1	EST_HUMAN	nu70708.s1 NCI_CGAP_Ab1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Akl repetitive element; contains element MER25 MER25 repetitive element;
8948	21387		5.71	3.4E-02	AA194308.1	EST_HUMAN	zfp04f11.s1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
8933	22182		0.53	3.4E-02	AB02719.1	EST_HUMAN	IPISGKPLPKVTLSDGVPKATMRFRTEITAENLTNLKESVTADAGRYEITANSSGTTKAFINIVLDRPG
365	13041		11.74	3.3E-02	AA308735.1	EST_HUMAN	PPT GPVMSDITEESVTLKWEPPKYDGGSQVTNYLLKRETSIAVWTEVSATVARTMMKVMKL ...;
1209	13809	26322	18.12	3.3E-02	AB035667.1	EST_HUMAN	cc88108.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1681	14273	26806	1.29	3.3E-02	AF110783.1	NT	z175e08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728188 3'
1775	14365		1.28	3.3E-02	AE000700.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
2131	14709		2.05	3.3E-02	R08112.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3408	18015	28404	0.85	3.3E-02	H02389.1	EST_HUMAN	Aquifex aeolicus section 32 of 108 of the complete genome
4256	14273	26808	2.91	3.3E-02	AF110783.1	NT	y25c09.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:127888 5'
4560	17149	28586	2.15	3.3E-02	6755862	NT	y25h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
6561	19159	31856	28.84	3.3E-02	BF245895.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6561	19159	31857	28.84	3.3E-02	BF245895.1	EST_HUMAN	Mus musculus tumor rejection antigen gp88 (Tra1). mRNA
8246	21772	34721	0.73	3.3E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8246	21772	34722	0.73	3.3E-02	BF115621.1	EST_HUMAN	801853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8345	21858	34807	0.59	3.3E-02	AA488202.1	EST_HUMAN	7m82d04.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9345	21859	34808	0.59	3.3E-02	AA488202.1	EST_HUMAN	7m82d04.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:3562423 3'
10491	22985		0.5	3.3E-02	H38109.1	EST_HUMAN	ad08709.s1 Soares NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:U70944_cds1
11000	23514	36548	3.5	3.3E-02	BF091107.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11932	24266		2.14	3.3E-02	T06545.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12089	24358		2.06	3.3E-02	M81890.1	NT	ad08709.s1 Soares NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:U70944_cds1
137	12802	25291	1.87	3.2E-02	AJ002005.1	NT	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
1165	13767	26277	19.04	3.2E-02	AF096275.1	NT	ye51111.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190889 3'
1165	13767	26278	19.04	3.2E-02	AF096275.1	NT	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
1808	14398	26943	1.36	3.2E-02	AF128894.1	NT	ye46911.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:121101 5'
2164	14741		1.35	3.2E-02	P28955	SWISSPROT	Human Interleukin 11 (IL11) gene, complete mRNA
2865	12802	25291	0.59	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3168	15782	28253	12.01	3.2E-02	BE867353.1	EST_HUMAN	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
							Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
							Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
							LARGE TEGUMENT PROTEIN
							Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
							601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'

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3776	16376	28842	1.3	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4299	16885		20.05	3.2E-02	X94788.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4882	17457	28909	3.35	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5728	18352	31055	1.45	3.2E-02	X68709.1	NT	S. griseocarinum whiG-Stv gene
5728	18352	31056	1.45	3.2E-02	X68709.1	NT	S. griseocarinum whiG-Stv gene
6846	18242	32045	2.59	3.2E-02	M32437.1	NT	Ratipolyomavirus left junction in cell line W88.14
6847	19243		27.51	3.2E-02	T88367.1	EST_HUMAN	y433h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6722	18316	32119	3.78	3.2E-02	AF173845.1	NT	Alu repetitive element/contains LTR1 repetitive element;
7739	20247	33140	0.85	3.2E-02	11424049	NT	Seguiturus oedipus tissue kallikrein gene, complete cds
8242	20783	33702	13.06	3.2E-02	6680565	NT	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8871	21410		0.89	3.2E-02	AF108718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9152	21687	34630	1.06	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9152	21687	34631	1.06	3.2E-02	A1278971.1	EST_HUMAN	qm17604.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9868	22464		4.05	3.2E-02	AA710795.1	EST_HUMAN	qm17604.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10260	22755	35743	0.85	3.2E-02	U96762.1	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1303	13897		1.8	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1348	13943	26486	1.28	3.1E-02	P18945	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1836	14520	27076	1.52	3.1E-02	6671584	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
2017	14599		1.14	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
5207	17772		0.87	3.1E-02	BE091869.1	EST_HUMAN	IL2-BT0733-130400-067-A08 BT0733 Homo sapiens cDNA
5331	17892		3.09	3.1E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5371	16916		0.58	3.1E-02	AU118006.1	EST_HUMAN	AU118006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
5468	18102	30421	1.13	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5563	18184		2.32	3.1E-02	AA278478.1	EST_HUMAN	zs81a08.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5829	18453	31176	0.8	3.1E-02	BF687742.1	EST_HUMAN	602068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
9844	22439	35417	3.63	3.1E-02	AF034776.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
12667	24737		2.24	3.1E-02	AW468414.1	EST_HUMAN	he3707.x1 NCI CGAP_GML1 Homo sapiens cDNA clone IMAGE:2921221 3'
1684	14257		2.3	3.0E-02	AF187125.1	NT	Ptychokeines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2621	15183	27749	0.9	3.0E-02	AA402242.1	EST_HUMAN	z05h03.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727263 5'
3823	18226	28704	1.24	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3714	16315	28763	3.07	3.0E-02	AF247844.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3808	16407		0.79	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-e08 ST0286 Homo sapiens cDNA
4021	16819		0.74	3.0E-02	AA364003.1	EST_HUMAN	EST174530 Pineal gland II Homo sapiens cDNA 5' end
5000	17573	30017	1.04	3.0E-02	BE782830.1	EST_HUMAN	601472331F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3875503 5'
5208	17773	30195	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5208	17773	30196	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5303	17865	30289	1.1	3.0E-02	BE968917.1	EST_HUMAN	601049872R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833928 3'
5560	18221		3.82	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6402	18005	31784	0.78	3.0E-02	N88615.1	EST_HUMAN	z338a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
6402	18005	31785	0.76	3.0E-02	N88615.1	EST_HUMAN	z338a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
6884	19819	32453	2.93	3.0E-02	AJ242906.1	NT	Cypinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
6887	19485	32308	3.15	3.0E-02	BE888948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6887	19485	32307	3.15	3.0E-02	BE888948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7131	19471	32290	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7131	19471	32291	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7282	19810	32898	1.32	3.0E-02	M86524.1	NT	Human dystrophin gene
7583	20088		0.78	3.0E-02	BF246381.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8575	21114	34033	0.79	3.0E-02	BF353889.1	EST_HUMAN	IL6-HT0704-290800-108-c04 HT0704 Homo sapiens cDNA
8728	21287		1.77	3.0E-02	AF275654.1	NT	Omithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	22851	35845	1.46	3.0E-02	AE001787.1	NT	Thermotoga maritima section 109 of 139 of the complete genome
10441	22835	35944	0.46	3.0E-02	Z21211.1	EST_HUMAN	HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11111	23821	36862	4.11	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11538	23866	37057	6.47	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCJ_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283
12043	25078	30515	2.58	3.0E-02	R32019.1	EST_HUMAN	Y63404.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12417	24670		18.42	3.0E-02	AW885565.1	EST_HUMAN	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
12480	25068		3.53	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2478	15487	27614	1.05	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3021	15637	28114	1.11	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680685 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3021	15637	28115	1.11	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3616	16219	28698	0.64	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4003	16601	28075	0.68	2.9E-02	H72803.1	EST_HUMAN	y407e10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5272	18016		62.36	2.9E-02	R09112.1	EST_HUMAN	y25c09.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
6213	18823	31594	1.31	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6434	19037	31824	6.5	2.9E-02	BF032233.1	EST_HUMAN	601452861F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856598 5'
7298	19824	32883	10.37	2.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3046830 5'
7455	19879	32845	0.87	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
7940	20482	33393	0.91	2.9E-02	AF128278.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
7940	20482	33394	0.91	2.9E-02	AF128278.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
8577	22077	35040	2.16	2.9E-02	AW875879.1	EST_HUMAN	GM3-PT0014-071298-051 c04 PT0014 Homo sapiens cDNA
9577	22077	35041	2.16	2.9E-02	AW875879.1	EST_HUMAN	GM3-PT0014-071298-051 c04 PT0014 Homo sapiens cDNA
9788	22286		0.59	2.9E-02	AW976597.1	EST_HUMAN	EST388708 MAGE resequences, MAGN Homo sapiens cDNA
10247	22742	35732	0.94	2.9E-02	AP000064.1	NT	Aeropyrum pernix genome DNA, section 7/7
10925	16219	28698	1.73	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12045	24979		1.86	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002862 5'
591	13221		0.89	2.9E-02	AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3414	18022	28502	1.82	2.9E-02	AF060603.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3414	18022	28503	1.82	2.9E-02	AF060603.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4401	18886		0.71	2.9E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5337	17698	30313	0.82	2.9E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-GUANINE TRANSGLYCOSYLASE
5679	18308	30802	11.28	2.9E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5'
6900	19634	32472	1.14	2.9E-02	T78960.1	EST_HUMAN	y21b08.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
8270	20811	33732	1.6	2.9E-02	AJ005820.1	NT	Crataegus sp. plantaginifolium mRNA for homeodomain leucine zipper protein (hb-1)
8947	21485	34407	0.74	2.9E-02	AA280782.1	EST_HUMAN	zs06c08.1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9135	21670	34612	0.91	2.9E-02	AF187872.1	NT	Canis porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9237	21763	34709	0.84	2.9E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
10498	22892	36002	1.81	2.9E-02	BF527244.1	EST_HUMAN	602039477F2 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177267 5'
3479	18085	28559	4.18	2.7E-02	AL161404.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4280	18686	29312	1.81	2.7E-02	NA17258.1	EST_HUMAN	y96h12.1 Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4280	18686	29313	1.91	2.7E-02	NA17258.1	EST_HUMAN	y96h12.1 Soares_multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:280487 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5833	18282	30734	1.11	2.7E-02	R12245.1	EST_HUMAN	yf33409.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS;
6061	18678	31420	0.7	2.7E-02	X61070.1	NT	T.aestivum pTTH20 mRNA for wheat type V fibrin
6713	19307		0.9	2.7E-02	X97580.1	NT	A.bisporus poka gene
7127	19467	32285	2.08	2.7E-02	AA93571.1	EST_HUMAN	o898h03.s1 Soares total_fetus_Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1624661 3'
8295	20836		1.21	2.7E-02	A1377036.1	EST_HUMAN	tc28g08.x1 Soares total_fetus_Nb2HF8 9w Homo sapiens cDNA clone IMAGE:2085982 3' similar to contains Alu repetitive element;
597	13228	25700	1.52	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2404	14972	27544	2.79	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2408	14974	27546	7.33	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hirc), mRNA
2408	14974	27547	7.33	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hirc), mRNA
2940	15558		1.17	2.6E-02	AF109008.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9a, NG22, G9, HSP70, HSP70, HSC70L, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5031	17605	30049	4.74	2.6E-02	L12032.1	NT	Chicken dorsalis-1 mRNA, complete cds
6224	17780	30208	1.58	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 228 of the complete chromosome 1
5254	17817	30241	2.34	2.6E-02	AW241154.1	EST_HUMAN	xs52b04.x1 NCJ CGAP Ser4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
6388	18972		6.32	2.6E-02	A1206030.1	EST_HUMAN	Q15041 HYPOTHETICAL PROTEIN KIAA0089;
6556	19154	31950	2.29	2.6E-02	BE821748.1	EST_HUMAN	qg27f11.x1 NCJ CGAP_K43 Homo sapiens cDNA clone IMAGE:1762317 3'
6815	19374	32402	0.75	2.6E-02	Z98094.1	NT	801493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6815	19574	32403	0.75	2.6E-02	Z98094.1	NT	Vaccinia virus ORF1L, strain W yeth
6880	19488	32310	6.45	2.6E-02	6981271	NT	Vaccinia virus ORF1L, strain W yeth
8442	20982	33687	0.77	2.6E-02	AA860948.1	EST_HUMAN	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
9282	21982	34827	1.41	2.6E-02	11432020	NT	sk22f04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1408719 3'
9630	22130	35094	0.8	2.6E-02	AF114952.1	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9630	22130	35095	0.8	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12538(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10302	22798	35787	4.1	2.6E-02	AL163303.2	NT	Saccharomyces dairenensis NRRL Y-12538(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
11265	23783		2.44	2.6E-02	AA278351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
11437	23887	36955	1.83	2.6E-02	AW500547.1	EST_HUMAN	zs84c02.r1 NCJ CGAP GC81 Homo sapiens cDNA clone IMAGE:704162 5'
11965	25060	30512	1.26	2.6E-02	BF343827.1	EST_HUMAN	UHF-BNO-ek-10-Q.UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077488 5'
12083	24354		1.29	2.6E-02	11422898	NT	602015501F1 NCJ CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150944 5'
557	13188	25668	1.76	2.5E-02	AJ783130.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
557	13188	25867	1.78	2.5E-02	A1783130.1	EST_HUMAN	on2800.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
842	13458	25867	18.88	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850885 3'
902	13516	28034	4.46	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850885 3'
2781	15344		2.84	2.5E-02	U12571.1	NT	Rattus norvegicus retpilin-3A mRNA, complete cds
2863	15589	28078	3.52	2.5E-02	X88897.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
2883	15589	28078	3.52	2.5E-02	X88897.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
4119	18005	28167	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4119	18005	28168	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4284	18870	28316	5.25	2.5E-02	AW582114.1	EST_HUMAN	h36h08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5889	18512	31238	0.7	2.5E-02	A1732778.1	EST_HUMAN	z63c10.j5 Scores_ova tumor N6HOT Homo sapiens cDNA clone IMAGE:810354 3'
6340	18948		4.9	2.5E-02	BE670128.1	EST_HUMAN	7a30a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1
6357	18981		4.3	2.5E-02	BE746888.1	EST_HUMAN	repetitive element ;
6478	19079	31802	0.72	2.5E-02	L28029.1	NT	601578393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
7680	20172	33058	1.52	2.5E-02	BF526722.1	EST_HUMAN	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7680	20172	33059	1.52	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4213408 5'
7820	20482	33368	0.48	2.5E-02	BE262488.1	EST_HUMAN	602070562F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4213408 5'
8759	21268	34219	0.83	2.5E-02	O81713	SWISSPROT	601108281F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
8894	21432	34355	0.45	2.5E-02	AW025821.1	EST_HUMAN	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8878	22473		0.6	2.5E-02	X71303.1	NT	wu08c10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516370 3'
10475	22869	35978	0.73	2.5E-02	A147815.1	EST_HUMAN	D. radiatum 28S ribosomal RNA, D2 domain
10689	23219	36231	2.04	2.5E-02	Q10335	SWISSPROT	qb22a08.x1 Scores_pregnant uterus N6-IPU Homo sapiens cDNA clone IMAGE:1686882 3'
10689	23219	36232	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;
10761	23285		4.04	2.5E-02	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-4
11802	24045		1.73	2.5E-02	AB007548.1	NT	Homo sapiens gene for LECT2, complete cds
11922	24963		3.33	2.5E-02	11433220	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12115	24855		1.53	2.5E-02	U60169.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12215	24438		2.17	2.5E-02	U60169.1	NT	Dicotyledonum putative protein kinase Mica (MicaA) gene, complete cds
12242	24454	30857	1.31	2.5E-02	BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3835513 3'
185	12848	28332	0.75	2.4E-02	AB78582.1	EST_HUMAN	tc72c07.x1 Scores_NIH-IMPu_S1 Homo sapiens cDNA clone IMAGE:2070158 3'
1642	14234	28768	2.08	2.4E-02	H65884.1	EST_HUMAN	y75f11.1 Scores_fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:21149 5'
2088	15457	27239	2.02	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	15457	27240	2.02	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4458	17044	29487	1.89	2.4E-02	J05110.1	NT	T. thermophilus calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4619	17202	29850	1.83	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4619	17202	29851	1.83	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6383	18967	31745	0.94	2.4E-02	W86980.1	EST_HUMAN	zh83h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7273	19801	32658	1.08	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX.T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7287	19815	32672	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7287	19815	32673	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7831	20373		0.89	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0188-230300-019-108 ST0188 Homo sapiens cDNA
7884	20426		0.8	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8379	20919		0.88	2.4E-02	H78376.1	EST_HUMAN	yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element ;
8488	21008	33925	10.74	2.4E-02	N68442.1	EST_HUMAN	z835g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294598 3' similar to gb K02809 RA7SR7K Rat (rRNA); contains A3R.b1 A3R repetitive element ;
8917	21455	34375	0.54	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
8939	21477	34398	0.75	2.4E-02	AA625680.1	EST_HUMAN	z181c06.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET XTR repetitive element ;
9720	22218	35193	2.76	2.4E-02	AV682954.1	EST_HUMAN	AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
9891	22388	36398	2.9	2.4E-02	AA483894.1	EST_HUMAN	AV682954 GK Homo sapiens cDNA clone GKCDSC03 5'
11447	23897	36962	1.9	2.4E-02	AF109905.1	NT	nt07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943883 similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
11447	23897	36963	1.9	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
11716	24127		3.56	2.4E-02	9627808	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11868	24222	31044	2.48	2.4E-02	6753635	NT	Bacteriophage bIL67, complete genome
11924	24259	31013	1.36	2.4E-02	BE928869.1	EST_HUMAN	Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA
11984	24284	30981	1.38	2.4E-02	U78167.1	NT	MRO-FT0175-310800-202-e08 FT0175 Homo sapiens cDNA
11984	24284	31025	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
11984	24284	31025	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12164	24404		8.87	2.4E-02	AB008588.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12191	24422		2.11	2.4E-02	N42880.1	EST_HUMAN	Y08A08.t1 Soares melanocyte 2N18HM Homo sapiens cDNA clone IMAGE:270610 5'
12197	24425		1.55	2.4E-02	BF078477.1	EST_HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5'
12362	24827	30795	1.48	2.4E-02	AA178983.1	EST_HUMAN	zp13h01.t1 Stratiagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608361 5'
1913	14498		5.46	2.3E-02	W05340.1	EST_HUMAN	z884g08.t1 Soares fetal_lung_Nb-L19W Homo sapiens cDNA clone IMAGE:288294 5'
1931	14515		21.88	2.3E-02	U94185.1	NT	4 Homo sapiens mammary tumor-associated protein INT8 (INT8) gene, exon 4
2053	14634	27205	0.86	2.3E-02	AW79355.1	EST_HUMAN	GM2-UM0038-280400-172-b11 UM0038 Homo sapiens cDNA
2389	14857	27529	2.31	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3745	16348	28814	6.21	2.3E-02	Z20377.1	EST_HUMAN	H5AACAADH.P, Human fetal Brain Whole tissue Homo sapiens cDNA
3777	16377		0.82	2.3E-02	L29429.1	NT	Carls beta-galactosidase-binding lectin (LGALS3) mRNA, 3'end
4230	16818	28268	0.75	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4230	16818	28267	0.75	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4511	17095	28542	1.21	2.3E-02	AW699107.1	EST_HUMAN	GM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4548	17130	28574	0.91	2.3E-02	BE935225.1	EST_HUMAN	GM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4548	17130	28576	0.91	2.3E-02	BE935225.1	EST_HUMAN	GM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4547	18006	28578	1.05	2.3E-02	AW693693.1	EST_HUMAN	xa25d08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4547	18006	28577	1.05	2.3E-02	AW693693.1	EST_HUMAN	xa25d08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4638	17280	28726	2.96	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
4638	17280	28727	2.96	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
5182	17748	30177	0.93	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-280100-011-a07 CN0051 Homo sapiens cDNA
5368	17828	30342	2.72	2.3E-02	AI038078.1	EST_HUMAN	ca21c10.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656878 3' similar to gb:X69908.maf1 ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (HUMAN);
5578	18208	30659	3.34	2.3E-02	U95903.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6733	19327	32132	4.43	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7056	18075	30428	0.88	2.3E-02	BE141475.1	EST_HUMAN	MR0-H10080-011089-002-c09 HT0080 Homo sapiens cDNA
7817	20360	33266	6	2.3E-02	U03610.1	NT	Human plectin (PLEC1) gene, exons 9-32, and complete cds
8407	20947	33867	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8407	20947	33868	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8630	21169	34085	0.83	2.3E-02	AI065380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8630	21169	34086	0.83	2.3E-02	AI065380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9065	21602	34532	0.81	2.3E-02	P41998	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9773	22271	35256	0.72	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9843	22438	35415	1.4	2.3E-02	AE000198.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9843	22438	35416	1.4	2.3E-02	AE000198.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10661	23193	36208	2.37	2.3E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
11828	24070		1.87	2.3E-02	AF158132.1	NT	Metapneus ensis fushi tarazu-factor 1 mRNA, complete cds
11846	24843		5.2	2.3E-02	BE278331.1	EST_HUMAN	601178658F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3548567 5'
12282	24485	30940	1.69	2.3E-02	BF528482.1	EST_HUMAN	602043829F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12282	24485	30941	1.59	2.3E-02	BF528482.1	EST_HUMAN	602043829F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12302	24562	30907	2.2	2.3E-02	U38394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12447	25100		3.04	2.3E-02	U11077.1	NT	Dicystatium discoidium extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12660	24940		1.73	2.3E-02	11428388	NT	Homo sapiens dead ringer (Drosophila) like 1 (DRIL1), mRNA
787	13388	25885	3	2.2E-02	AF018287.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1783	14373		1.03	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2059	14639	27212	1.33	2.2E-02	Z82001.1	NT	S. pneumoniae pcpA gene and open reading frames
3482	16088		2.1	2.2E-02	AA577785.1	EST_HUMAN	nt24804.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3708	16309		3.58	2.2E-02	AF063094.1	NT	Infectious burial disease virus segment B strain IL4 VP1 gene, complete cds
3920	16518	28984	1.11	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3932	16580	28062	0.85	2.2E-02	Z74283.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
5225	17780	30209	0.92	2.2E-02	Z73587.1	NT	S. cerevisiae chromosome XVI reading frame ORF YPL241c
7294	18822	32881	3.52	2.2E-02	AV688721.1	EST_HUMAN	AV688721 GKB Homo sapiens cDNA clone GKBAND003 3'
8312	20853	33778	2.58	2.2E-02	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8312	20853	33779	2.56	2.2E-02	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8744	21283	34205	0.75	2.2E-02	XT9488.1	NT	P. vulgaris alpha tub 2 mRNA
9574	22074	35036	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9574	22074	35037	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9604	22104	35068	1.88	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9604	22104	35067	1.88	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10106	22801		0.86	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12120	24378		3.95	2.2E-02	AA503553.1	EST_HUMAN	nc47907.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:800541 3' similar to contains Alu repetitive element

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13077		4.45	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
474	13107		5.21	2.1E-02	AF029728.1	NT	Dictyostelium discoideum Histidine kinase C (dhkc) mRNA, complete cds
1308	13800	26420	8.16	2.1E-02	U72073.1	NT	Bacillus subtilis cotLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1430	14022	26550	1.46	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1430	14022	26551	1.46	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
2642	13426	25934	3.37	2.1E-02	N29268.1	EST_HUMAN	y43h07.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264541 5'
3184	14660	27231	0.93	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3184	14660	27231	0.93	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3643	16248	27232	0.93	2.1E-02	AA481271.1	EST_HUMAN	z63509.1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:768121 5'
4211	16800	28248	0.77	2.1E-02	Z74283.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
4398	16883	28428	0.93	2.1E-02	BF343655.1	EST_HUMAN	802015306F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4131161 5'
4540	17124	28568	1.64	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4552	17135	28583	1.3	2.1E-02	A768127.1	EST_HUMAN	wg81d11.x1 Soares NSF F8 9W OT PA_P S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4820	17398	28652	5.95	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4836	17414	28687	0.57	2.1E-02	AA695737.1	EST_HUMAN	ag55g12.a1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4944	17519	28961	0.93	2.1E-02	A1823432.1	EST_HUMAN	wh54e05.x1 NCI_CGAP_Ku411 Homo sapiens cDNA clone IMAGE:2394528 3'
5321	17883		1.52	2.1E-02	S82470.1	NT	BB1-malignant cell expression-enhanced gene/tumor progression-enhanced gene (human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt)
5821	18445	31167	0.9	2.1E-02	AW378529.1	EST_HUMAN	GM4-HT0244-111169-040-h05 HT0244 Homo sapiens cDNA
7126	19466	32284	0.74	2.1E-02	BF086198.1	EST_HUMAN	QV3-GN0038-120900-328-a12 GN0038 Homo sapiens cDNA
8456	20998	33914	0.66	2.1E-02	9780238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9422	21831	34879	0.56	2.1E-02	AA984288.1	EST_HUMAN	em83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9549	22049	35010	2.41	2.1E-02	AJ243213.1	NT	Alu repetitive element:contains element MER11 repetitive element;
9549	22049	35011	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9894	22391	35369	1.22	2.1E-02	L26824.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9973	22468	35452	0.57	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae integrase, excisionase, repressor protein, release, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
12089	18030		11.53	2.1E-02	Y19213.1	NT	em83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
12141	24839	30798	1.31	2.1E-02	L34170.1	NT	Alu repetitive element:contains element MER11 repetitive element;
12552	24655	30871	16.83	2.1E-02	AF183913.1	NT	Homo sapiens putative psfH-iba pseudogene for hair keratin, exons 2 to 7
						NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
						NT	Azospirillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20	12689	25155	1.34	2.0E-02	BF002832.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3306888 3' similar to contains MER1.13
21	12700	25156	9.6	2.0E-02	AW865565.1	EST_HUMAN	MER1 repetitive element:
280	12837	25422	2.31	2.0E-02	6753635	NT	QV4-NN0038-270-400-187-H05 NN0038 Homo sapiens cDNA
317	12871	25480	2.42	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus Dnrb homolog 1 (E. coli) (Dnrb1), mRNA
831	13448	25955	1.2	2.0E-02	6753635	NT	sa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1126	13729	26240	1.32	2.0E-02	AL098805.1	NT	Mus musculus Dnrb homolog 1 (E. coli) (Dnrb1), mRNA
1241	13839	26356	0.79	2.0E-02	8822391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo sapiens
1241	13839	26357	0.79	2.0E-02	8822391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1814	14488	27053	2.3	2.0E-02	8822453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1814	14489	27054	2.3	2.0E-02	8822453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2824	15378		3.19	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3115	12689	25155	1.84	2.0E-02	BF002832.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3306888 3' similar to contains MER1.13
3178	15791		1.38	2.0E-02	7305474	NT	MER1 repetitive element:
3284	15876		1.57	2.0E-02	AF085688.1	NT	Mus musculus soma domain, transmembrane domain (TM), and cytoplasmic domain, (sennaphorin) 68
4078	16874	28135	1.54	2.0E-02	M18095.1	NT	(Sennaphorin), mRNA
5268	17830	30255	1.12	2.0E-02	AF188368.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
6056	18873	31414	0.87	2.0E-02	L36321.2	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7553	20072	32847	1.28	2.0E-02	AP000004.1	NT	Alcalymyces capsulatus catalase isozyme A (CATA) mRNA, complete cds
7553	20072	32848	1.28	2.0E-02	AP000004.1	NT	Dichostelium discoideum class VII unconventional myosin (myosin) gene, complete cds
9781	22289		2.5	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10284	22759	35746	1.63	2.0E-02	A1840342.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10522	23060	36070	2.05	2.0E-02	Z73986.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
11250	23780	36836	2.85	2.0E-02	D88184.1	NT	wt17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315 3'
11530	23978	37047	1.58	2.0E-02	10947055	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 83/162
11530	23978	37048	1.58	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxysteroid/17,20-lyase, complete cds
11654	18034	30494	1.91	2.0E-02	AA456538.1	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12138	15376		1.94	2.0E-02	AL161532.2	NT	sa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12635	24711		8.4	2.0E-02	T80037.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
722	13342	25832	1.93	1.8E-02	AA572764.1	EST_HUMAN	sa15b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5'
							repetitive element:

Table 4

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1688	14251	28785	0.96	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2083	14684	27234	1.98	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2083	14684	27235	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2549	15113	27683	0.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
2630	15546	28021	8.7	1.9E-02	AA713856.1	EST_HUMAN	nm04805.s1 NCL_CGAP_S51 Homo sapiens cDNA clone IMAGE:1298337 3'
2680	15596	28076	1.56	1.9E-02	AV648696.1	EST_HUMAN	AV648696 GLC Homo sapiens cDNA clone G108LH07 3'
3288	15909		0.75	1.9E-02	AB033611.1	NT	Urethrichus talpoides mitochondrial gene for cytochrome b, complete cds
3671	16272		1.09	1.9E-02	N52250.1	EST_HUMAN	YZ28802.s1 Soares_multiple sclerosis_2NtHMSP Homo sapiens cDNA clone IMAGE:284331 3'
3766	16367		6.81	1.9E-02	BE738098.1	EST_HUMAN	601572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3836564 5'
4121	16714	28170	1.48	1.9E-02	AF141940.1	NT	Mycoplasma lititans VHA1 precursor (vha1) and VHA2 precursor (vha2) genes, partial cds
4271	16857	28305	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4271	16857	28306	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4639	17221	28675	3.21	1.9E-02	AI452869.1	EST_HUMAN	U46404.x1 Soares_NSF F8 9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Abi repetitive element;
5157	15113	27693	2.73	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5519	18151	30585	0.83	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
5660	18287	30785	1.38	1.9E-02	L47572.1	NT	Meleagris gallopavo paracetamol-2 (PON2) mRNA, complete cds
5958	18591		0.81	1.9E-02	AB019607.1	NT	Drosophila karekai gene for glyceral-3-phosphate dehydrogenase, complete cds
7158	18680	32534	1.41	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7168	18680	32535	1.41	1.9E-02	U18241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8506	21045		1.06	1.9E-02	AL162764.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9254	21780	34732	0.94	1.9E-02	BF316128.1	EST_HUMAN	601886130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9628	22129	35093	0.86	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9958	22453	35435	1.04	1.9E-02	BF696832.1	EST_HUMAN	601852385F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4078253 5'
10054	22549	35543	0.49	1.9E-02	N39160.1	EST_HUMAN	yy46h08.s1 Soares_multiple sclerosis_2NtHMSP Homo sapiens cDNA clone IMAGE:2766339 3'
10151	22648	35639	0.56	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 2027, 2530000-2644704
11878	24847	30801	4.29	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gelsin mRNA, complete cds
12477	24818		1.27	1.9E-02	L11068.1	NT	Candida albicans lambda Ca3B fragment
12587	24680	30879	1.7	1.9E-02	X68271.1	NT	H. sapiens MUC18 gene exon 16
368	13017	25500	1.84	1.9E-02	AW771104.1	EST_HUMAN	hm5206.x1 NCL_CGAP_C017 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
714	13335	25821	2.26	1.9E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1202	13802	26315	1.51	1.9E-02	X17864.1	NT	601884329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1484	14077	26615	2.3	1.9E-02	AF243382.1	NT	H. frandisci mRNA for myelin basic protein (MBP)
							Drosophila melanogaster cytoplasmic protein encare (enc) mRNA, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2704	15261	27828	1.22	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PAO1, section 105 of 528 of the complete genome
3247	15859		0.72	1.8E-02	A1805829.1	EST_HUMAN	hs2a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3958	16554	29023	1.07	1.8E-02	AW878122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3956	16554	29024	1.07	1.8E-02	AW878122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4160	16752		1.41	1.8E-02	AA861446.1	EST_HUMAN	af24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408835 3'
4521	17105	28551	1.67	1.8E-02	AW836363.1	EST_HUMAN	QV4-OT0021-301289-071-b11 DT0021 Homo sapiens cDNA
5090	17663	30103	1.06	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6901	19835	32473	4.27	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5REGION
8071	20613	33527	0.81	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8404	20944	33866	0.91	1.8E-02	AW80537.1	EST_HUMAN	QV2-NN1073-220400-158-P09 NN1073 Homo sapiens cDNA
8449	20988	33907	0.75	1.8E-02	6878943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9413	21922	34870	0.45	1.8E-02	BF241824.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9413	21822	34871	0.45	1.8E-02	BF241824.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9560	22080		2.41	1.8E-02	AA897543.1	EST_HUMAN	af2709.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394821 3' similar to gbl:11672 ZINC FINGER PROTEIN 91 (HUMAN);
9975	22470	35453	1.72	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869863 5'
10126	22621	35611	1.12	1.8E-02	X98933.1	NT	L. stagnalis mRNA for myomodulin neuropeptide precursor
11313	23011	36019	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11313	23011	36020	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11480	23630	37001	1.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (817)
11489	23638	37008	3.88	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
839	13552	28068	0.77	1.7E-02	BE394889.1	EST_HUMAN	601310628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1827	14416	26963	1.89	1.7E-02	AW573183.1	EST_HUMAN	hf34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1827	14416	26964	1.89	1.7E-02	AW573183.1	EST_HUMAN	hf34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element;
1912	14497		3.27	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2159	14736		12.81	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugurin28, complete cds
2332	14903	27474	4.64	1.7E-02	S74186.1	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
3028	15944	28123	0.84	1.7E-02	A1147615.1	EST_HUMAN	qf22a08.x1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:1686982 3'
3582	16166		4.33	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NC1_CGAP RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
3687	16268		0.65	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4248	16836		1.08	1.7E-02	AA069818.1	EST_HUMAN	ac19f04.s1 Stratiogene ovary (#937217) Homo sapiens cDNA clone IMAGE:856827 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4278	16884		2.52	1.7E-02	R02506.1	EST_HUMAN	y86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4551	17134	28582	0.61	1.7E-02	A1308279.1	EST_HUMAN	qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4826	17209	29859	1.44	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element;
4824	17402	29855	1.78	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4838	17511		5.59	1.7E-02	A015076.1	EST_HUMAN	ov51a02.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1840858 3'
6274	18882	31660	1.8	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387113 3' similar to contains Alu repetitive element;
6693	18289	32091	1.98	1.7E-02	A038280.1	EST_HUMAN	oy65p03.x1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
7112	19452	32268	1.05	1.7E-02	AF180930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7255	19783	32639	1.96	1.7E-02		NT	Homo sapiens nebulin (NEB), mRNA
7394	19919	32763	1.07	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7394	19919	32764	1.07	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7724	20232		1.7	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
8357	20296	33186	0.97	1.7E-02	U21854.1	NT	Caenorhabditis elegans CCAF1 protein gene, complete cds
8615	22115	35079	1.31	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434f0314_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434f0314 5'
12482	25025	30619	3.35	1.7E-02	AW903482.1	EST_HUMAN	GM4-NN1030-040400-130-406 NN1030 Homo sapiens cDNA
537	13168		3.38	1.6E-02	AL021828.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1696	14289	26825	1.05	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue
2280	14864	27438	2.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2280	14864	27439	2.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2600	15182	27730	0.98	1.6E-02	AJ008345.1	NT	Homo sapiens KVLQ11 gene
2668	15227	27799	1.82	1.6E-02	AA494872.1	EST_HUMAN	ne81d06.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2718	15275		1.14	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3052	15668	28146	0.73	1.6E-02	AF112282.1	NT	Lassaea sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3578	18182	28684	5.61	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3914	16512	28974	0.82	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	16842		1.77	1.0E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4388	16974	28424	1.26	1.0E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-07 PT0012 Homo sapiens cDNA
4801	17476	28832	3.89	1.0E-02	AJ769132.1	EST_HUMAN	wg34009.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2369889 3'
5308	17868		0.61	1.0E-02	N80156.1	EST_HUMAN	zaf6607.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:297444 3'
5807	18432	31153	1.26	1.0E-02	6871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6752	18345	32152	2	1.0E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7011	19509	32329	1.22	1.0E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7011	19509	32330	1.22	1.0E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7896	20205	33092	0.9	1.0E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8084	20808	33518	0.78	1.0E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8119	20860		1.55	1.0E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
9653	22448		2.32	1.0E-02	AF079784.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10317	22811	36806	1.17	1.0E-02	AA572818.1	EST_HUMAN	nf16g03.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT
10317	22811	36806	1.17	1.0E-02	AA572818.1	EST_HUMAN	P28294 TELOKIN. [1]:
10786	24800	36319	2.38	1.0E-02	Z94828.1	NT	nf10g03.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT
11080	23602	36640	2.5	1.0E-02	AL161508.2	NT	G.gallus microsatellite DNA (LE10260 (=T16HIE11))
11090	23602	36841	2.5	1.0E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11385	23837	36869	2.38	1.0E-02	AJ375358.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11855	14864	27438	3.63	1.0E-02	Q84176	SWISSPROT	qz06a10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
11855	14864	27439	3.63	1.0E-02	Q84176	SWISSPROT	LIVER CARBOXYLTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
781	13400		51.07	1.5E-02	8923734	NT	LIVER CARBOXYLTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2187	14763	27332	4.36	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
2219	14784	27367	1.76	1.5E-02	AL161504.2	NT	y27807.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
3097	15712	28183	0.99	1.5E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3097	15712	28184	0.99	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3787	16387	28853	0.86	1.5E-02	BF082942.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
4222	16810	29257	0.86	1.5E-02	AA160987.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
5160	17729		0.78	1.5E-02	M13879.1	NT	zq40g10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:832228 5'
5403	17863	30374	1.14	1.5E-02	AW770341.1	EST_HUMAN	Human Interleukin 2 gene, exons 1 and 2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6436	18039	31828	1.31	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN G18B11.04 IN CHROMOSOME 1
7360	18888		1.62	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7432	18856	32821	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
7816	20358	33265	1.44	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7822	20364	33273	4.16	1.5E-02	11417739	NT	Homo sapiens vally-HRNA synthetase 2 (VARH2), mRNA
8764	21303	34224	1.62	1.5E-02	BF345554.1	EST_HUMAN	802019135F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504 5'
8389	21812		0.51	1.5E-02	AF068774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9490	21949	34885	1.64	1.5E-02	D44608.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9725	22223	35199	1.08	1.5E-02	R32867.1	EST_HUMAN	YH54b10.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133531 5'
9725	22223	35200	1.08	1.5E-02	R32867.1	EST_HUMAN	YH54b10.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133531 5'
10687	23227		1.71	1.5E-02	D28547.1	NT	Rice gene for thiodiosin h, complete cds
11047	23580	36587	2.32	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12078	24892		2.26	1.5E-02	AW750834.1	EST_HUMAN	RC4-GN0049-140100-011-CT11 CN0049 Homo sapiens cDNA
12636	24712		1.55	1.5E-02	A1763127.1	EST_HUMAN	w08h03.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2389463 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element;
442	13075		1.41	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AF39, section 58 of 94 of the complete genome
1157	13780	26270	4.22	1.4E-02	7705880	NT	Homo sapiens NESH protein (LOC51225), mRNA
1289	13893		1.28	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1341	13836		3.36	1.4E-02	U87779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1564	14156		1.08	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAF-H11 5'
3249	15861	28342	1.81	1.4E-02	AF160688.2	NT	Bifidobacterium longum Nac/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3445	16053	28530	0.96	1.4E-02	AW074212.1	EST_HUMAN	xb08d08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3531	16136	28616	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3531	16136	28617	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3571	16175	28657	0.88	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F-12), mRNA
3717	16318	28788	6.27	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4567	17170	28614	8.86	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG cDNAs, MAGG Homo sapiens cDNA
4567	17170	28615	8.86	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG cDNAs, MAGG Homo sapiens cDNA
4767	17348	28787	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4767	17348	28788	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
5003	17576	30020	6.84	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5003	17576	30021	6.64	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3942280 5'
6547	19145	31841	4.61	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NC1_CGAP_B2 Homo sapiens cDNA clone IMAGE:1028980 3' similar to contains Alu repetitive element;
6547	19145	31842	4.61	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NC1_CGAP_B2 Homo sapiens cDNA clone IMAGE:1028980 3' similar to contains Alu repetitive element;
8081	20623		1.97	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8829	21368	34292	1.24	1.4E-02	AB1702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9082	21618	34553	0.99	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9321	21835	34788	2.48	1.4E-02	BE544661.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10451	22945		0.81	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11765	24156	36772	12.79	1.4E-02	X60456.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12134	24387		3.62	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12433	24574		2.32	1.4E-02	11426988	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1905	14490		1.18	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
1998	14580	27138	2.55	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3250	15862	26343	1.91	1.3E-02	BF687081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3250	15862	26344	1.91	1.3E-02	BF687081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
4041	16639		1.66	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
							Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmq28orf
5455	18090	30447	1.46	1.3E-02	AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmq28orf
5455	18090	30448	1.46	1.3E-02	AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmq28orf
6312	18919	31684	1.4	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6345	18951	31728	0.88	1.3E-02	M82862.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7041	18061	30449	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
7041	18061	30450	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
							ow06p05.x1 Soares_parathyroid_tumor_Nb1-IPA Homo sapiens cDNA clone IMAGE:1846072 3' similar to contains Alu repetitive element;
7578	20094	32971	4.79	1.3E-02	AJ031593.1	EST_HUMAN	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
8418	20958	33878	1.03	1.3E-02	AF156991.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10108	22603	35563	1.71	1.3E-02	M63707.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10178	22673	35665	0.77	1.3E-02	AE001304.1	NT	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10871	23392	36408	4.07	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10871	23392	36407	4.07	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11742	25051		2.12	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12139	25039		2	1.3E-02	Z98117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2598451 to 2612870
12248	24457		2.77	1.3E-02	9833088	NT	Human herpesvirus 6B, complete genome
12438	24813		47.13	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
228	12888		20.25	1.2E-02	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, PIP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
377	13025	25511	3.79	1.2E-02	AA058289.1	EST_HUMAN	z85g01.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element:
478	13111	25601	1.71	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3REGION
768	13387	25888	8.37	1.2E-02	A1183522.1	EST_HUMAN	q488a12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1794870 3' similar to contains L1.L1 L1 repetitive element:
2221	14798	27369	1.85	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2223	14798	27371	1.15	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2487	15052	27824	1	1.2E-02	AW172350.1	EST_HUMAN	X37609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2542	15106	27878	1.05	1.2E-02	BE58310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454808 5'
2542	15106	27879	1.05	1.2E-02	BE58310.1	EST_HUMAN	601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454808 5'
3135	15749	28413	7.56	1.2E-02	AA075418.1	EST_HUMAN	zrn86c03.r1 Stratagene ovarian cancer (8637219) Homo sapiens cDNA clone IMAGE:545020 5'
3327	15837	28413	2.02	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:138903 3'
4838	17513	28659	0.61	1.2E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5040	17613	30057	2.65	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5194	17759		1.61	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster Cplbq1 mRNA, partial cds
5244	17808	30230	2.01	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5827	18548	31275	1.76	1.2E-02	D76589.1	NT	Rana rugosa mRNA for calcitriol, complete cds
7078	19650	32489	5.21	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7334	19861	32725	1.06	1.2E-02	H02197.1	EST_HUMAN	y94h12.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:150685 3'
7353	19879	32744	19.46	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBHC09 5'
7839	20481	33382	2.3	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8133	20674	33585	1.2	1.2E-02	AF183612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8133	20674	33586	1.2	1.2E-02	AF183612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8822	21361		1.06	1.2E-02	T76987.1	EST_HUMAN	yd72c08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9557	22057	35018	2.7	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9588	22089	35053	1.74	1.2E-02	AJ248003.1	NT	Homo sapiens Spast gene for spastin protein
12446	24582		4.73	1.2E-02	C18118.1	EST_HUMAN	C18118 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-557/G08 5'
1312	13906	28428	1.49	1.1E-02	AA070364.1	EST_HUMAN	zmf69e11.s1 Stratiogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530824 3'
1744	14334	28880	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1744	14334	28881	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2082	14863	27253	5.42	1.1E-02	BF345263.1	EST_HUMAN	602018037.F1 NCJ_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153808 5'
2802	15519		4.2	1.1E-02	N88523.1	EST_HUMAN	z840e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285040 5'
3575	16179	28682	2.88	1.1E-02	A1653508.1	EST_HUMAN	1q55b10.x1 NCJ_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
4084	16889		2.1	1.1E-02	BE144637.1	EST_HUMAN	Q22889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4183	16773		0.81	1.1E-02	AW813786.1	EST_HUMAN	PK3-HT0175-300889-001-J06 HT0175 Homo sapiens cDNA
4856	17531	28973	2.09	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp566E0824_s1 588 (synonym: hube1) Homo sapiens cDNA clone DKFZp566E0824
							Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GhrR (ghrR), glutamine synthetase (ghsA), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), YnaK (ynbK), YnaL (ynbL), YnaM (ynbM), YnaN (ynbN), YnaO (ynbO), YnaP (ynbP), YnaQ (ynbQ), YnaR (ynbR), YnaS (ynbS), YnaT (ynbT), YnaU (ynbU), YnaV (ynbV), YnaW (ynbW), YnaX (ynbX), YnaY (ynbY), YnaZ (ynbZ), YnaA (ynbA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), YnaK (ynbK), YnaL (ynbL), YnaM (ynbM), YnaN (ynbN), YnaO (ynbO), YnaP (ynbP), YnaQ (ynbQ), YnaR (ynbR), YnaS (ynbS), YnaT (ynbT), YnaU (ynbU), YnaV (ynbV), YnaW (ynbW), YnaX (ynbX), YnaY (ynbY), YnaZ (ynbZ)
6298	18906	31677	1.03	1.1E-02	U68480.1	NT	RC1-HT0256-100300-016-H07 HT0256 Homo sapiens cDNA
7584	20108	32883	2.55	1.1E-02	BE149811.1	EST_HUMAN	METALLOTHIONEIN (MT-1/MT-2)
8188	20740	33852	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8188	20740	33853	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8574	21113	34032	0.84	1.1E-02	AW588180.1	EST_HUMAN	QV3-BN0045-220300-128-H02 BIN0045 Homo sapiens cDNA
8756	21285	34215	0.69	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NH4040
8833	21372	34297	7.39	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9842	22340	35322	2.07	1.1E-02	AA082578.1	EST_HUMAN	z124e01.r1 Stratiogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10006	22501	35492	3.79	1.1E-02	AA314885.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10858	23379	36398	3.88	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11702	24115		2.67	1.1E-02	AA688239.1	EST_HUMAN	ab77111.s1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12512	16773		1.87	1.1E-02	AW813796.1	EST_HUMAN	Alu repetitive element
7	12888	25144	6.97	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1570	14163	26894	2.93	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111089-003-e10 CT0176 Homo sapiens cDNA
2606	15168		1.9	1.0E-02	AA368389.1	EST_HUMAN	CM2-HT0177-041089-017-h12 HT0177 Homo sapiens cDNA
3126	15740	28209	3.7	1.0E-02	BE835556.1	EST_HUMAN	cc-22f08.s1 NCJ_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1350495 3'
3302	15913	28391	1.41	1.0E-02	BE868688.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
							601849867.R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	16162		0.83	1.0E-02	AW846621.1	EST_HUMAN	MRO-CT0060-081089-003-H10 CT0060 Homo sapiens cDNA
3560	16548	29016	0.68	1.0E-02	A095098.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4881	17488	29921	5.12	1.0E-02	6753521	NT	Mus musculus corticotroph releasing hormone receptor 2 (Chr2), mRNA
4970	17544	29888	5.03	1.0E-02	R08587.1	EST_HUMAN	Y554h01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:188633 5'
5221	17788	30204	1.01	1.0E-02	AF218910.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 25 and complete cds, alternatively spliced
5317	17879	30288	0.98	1.0E-02	P06599	SWISSPROT	EXTENSIN PRECURSOR
5394	17952		16.85	1.0E-02	AV723678.1	EST_HUMAN	AV723678 HTB Homo sapiens cDNA clone HTBAPF08 5'
5445	18000		3.87	1.0E-02	D34632.1	NT	Arabidopsis thaliana acc2 gene for acetyl-CoA carboxylase, partial cds
5810	18239	30888	0.8	1.0E-02	H52881.1	EST_HUMAN	YU36h11.1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:235941 5'
5921	18543	31269	0.7	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-A-Tc4 (Nfat4) gene, exons 1 and 2
6264	18872	31842	0.89	1.0E-02	AF267303.1	NT	Mus musculus synaptotagmin II (Syn2) gene, complete cds
8328	18934	31709	2.67	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-H01 BT0358 Homo sapiens cDNA
8328	18934	31710	2.67	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-H01 BT0358 Homo sapiens cDNA
8859	18583	32425	2.22	1.0E-02	Z28842.1	NT	Z.mays U3snRNA pseudogene
8240	20781		0.46	1.0E-02	Z28107.1	NT	S.cerevisiae chromosome XI reading frame ORF_YKL107w
9314	21828	34778	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9314	21828	34779	4.28	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11143	23651		2.17	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11248	23778	36833	2.02	1.0E-02	AV780016.1	EST_HUMAN	AV780016 MDS Homo sapiens cDNA clone MDSBDC10 5'
11785	25110		2.16	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68)
11847	24862	30705	4.84	1.0E-02	AW835521.1	EST_HUMAN	RC2-DT0007-120200-018-H02 DT0007 Homo sapiens cDNA
11861	24822		6.07	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12254	24898		1.53	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12422	24882		4.42	1.0E-02	X62854.1	NT	H.sapiens gene for Me491/CD63 antigen
928	13538	26857	3.16	9.0E-03	A1798128.1	EST_HUMAN	WH4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1307	13901		1.28	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element
2439	15006	27578	3.82	9.0E-03	AL161558.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2449	15016	27588	0.87	9.0E-03	AF068634.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2831	15547	28022	0.61	9.0E-03	A1251744.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2831	15547	28023	0.61	9.0E-03	A1251744.1	EST_HUMAN	qf80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3731	16332	28798	0.8	9.0E-03	J05184.1	NT	qf80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5978	18598		1.17	9.0E-03	A1809782.1	EST_HUMAN	S.acidocalcaris thermopsis gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6741	19335		4.24	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834762 5'
7487	20010	32876	0.73	9.0E-03	8822570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
7816	20359		0.83	9.0E-03	AL038981.1	EST_HUMAN	DKFZp434L0412_1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434L0412 5'
8191	20732		0.56	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9759	22257	35240	0.5	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
9778	22274	35258	1.26	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10885	23386		1.8	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10891	23412	36431	1.71	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632161 5'
11505	23954	37022	1.58	9.0E-03	L11144.1	NT	Homo sapiens progesterone (GAL1) gene, exons 1, 2, and 3
11505	23954	37023	1.58	9.0E-03	L11144.1	NT	Homo sapiens progesterone (GAL1) gene, exons 1, 2, and 3
12001	25111		1.79	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA
12221	25105		36.8	9.0E-03	BE346385.1	EST_HUMAN	hw17b09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12319	24509	30943	1.38	9.0E-03	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
12539	24649		31.67	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA
527	13159		2.87	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.a1 Soares_pituitary_gland_N3-HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains
1028	13637	28152	35.57	8.0E-03	AF106856.1	NT	Alu repetitive element
2203	14779	27351	1.26	8.0E-03	AL163283.2	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
3351	15659	28436	0.99	8.0E-03	BE171225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C063
3404	16013	28492	0.89	8.0E-03	AJ131016.1	NT	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3738	16339	28805	1.77	8.0E-03	P32844	SWISSPROT	Homo sapiens SCL gene locus
3738	16339	28806	1.77	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4343	16930	29371	1.19	8.0E-03	BE840049.1	EST_HUMAN	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4472	17058	29505	6.36	8.0E-03	BF363327.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
5378	17937	30350	1.02	8.0E-03	U02970.1	NT	CMA-NN0119-300600-223-505 NN0119 Homo sapiens cDNA
5410	17967	30376	0.86	8.0E-03	P01871	SWISSPROT	Prototheca wickerhamii 283-11 complete mitochondrial DNA
5714	18340	30848	2.89	8.0E-03	AF110520.1	NT	IG MU CHAIN C REGION
6346	24762	31730	1.34	8.0E-03	AF000002.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, taphasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6846	19436	32251	4.45	8.0E-03	P55577	SWISSPROT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (27)
6909	19497		1.72	8.0E-03	V01106.1	NT	PROBABLE PEPTIDASE Y4NA
7259	19787	32843	1.8	8.0E-03	MF17197.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
						NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7547	20067		1.84	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8816	21355	34279	0.62	8.0E-03	P08160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
8841	21380	34304	3.73	8.0E-03	AW808692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
8910	21448	34370	0.68	8.0E-03	9789956	NT	MR1-ST0111-111189-011-106 ST0111 Homo sapiens cDNA
9859	22356		4.78	8.0E-03	BE086509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
10984	23385		3.01	8.0E-03	Z49652.1	NT	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
11259	23789	36845	1.97	8.0E-03	AA828817.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR152w
11259	23789	36846	1.97	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11562	24009	37079	4.96	8.0E-03	AF064589.1	NT	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11713	24123		2.81	8.0E-03	M69035.1	NT	Homo sapiens melanoma-associated antigen (IMAGE-C1) gene, complete cds
11761	24154		5.99	8.0E-03	AB039161.1	NT	Oryzias latipes curvulus eIF-2a kinase mRNA, complete cds
723	13343	25833	14.03	7.0E-03	AF097183.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
723	13343	25834	14.03	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1012	13622	26137	5.78	7.0E-03	AF243376.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1155	13758	26268	3.21	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1408	14001		1.28	7.0E-03	Q61060	SWISSPROT	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1439	14032	26560	4.09	7.0E-03	AA668286.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/TF TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFN-2)
1550	14142	26875	3.14	7.0E-03	AW303596.1	EST_HUMAN	ab78509.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2297	15462	27447	2.12	7.0E-03	P04929	SWISSPROT	xt2102.x1 Soares_NFL_T_G8C.S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3614	16217	28696	0.58	7.0E-03	A1150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3830	16430	28902	0.91	7.0E-03	AW444463.1	EST_HUMAN	q34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3885	16483	28945	1.01	7.0E-03	AF196344.1	NT	UHH-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4091	16430	28992	0.63	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4704	17296		1.1	7.0E-03	AW630886.1	EST_HUMAN	UHH-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
5125	17697		2.08	7.0E-03	AL163278.2	NT	h88905.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2698966 5'
5685	18605		0.79	7.0E-03	H71108.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6280	24760		5.32	7.0E-03	AW861059.1	EST_HUMAN	y82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
6456	19057	31842	1.45	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6658	18254	32056	2.98	7.0E-03	AA327126.1	EST_HUMAN	z633f10.r1 Soares_fetal_heart_NH-H16W Homo sapiens cDNA clone IMAGE:342475 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6881	18277	32080	0.92	7.0E-03	BE857385.1	EST_HUMAN	7q34b10.x1 NC1_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR-Q13387
7139	19519	32341	2.12	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.12 TAR1 repetitive element;
7528	20049	32921	5.78	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7528	20049	32922	5.78	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33238	0.54	7.0E-03	AJ28043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33239	0.54	7.0E-03	AJ28043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8055	20587	33504	2.36	7.0E-03	BE175887.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8318	21832		0.6	7.0E-03	AF111188.2	NT	RCS-HT0582-160300-011-002 HT0582 Homo sapiens cDNA
8513	22013	34972	0.87	7.0E-03	NS2378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8636	22136	35101	2.48	7.0E-03	P48982	SWISSPROT	yy49c10.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248068 3' similar to contains
8636	22136	35102	2.48	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10207	22702		0.89	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10381	22875		0.93	7.0E-03	AI799794.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10708	23235	36248	3.48	7.0E-03	AB008852.1	NT	AV687379 GKC Homo sapiens cDNA clone GKCAF007 5'
10780	23304	36311	1.61	7.0E-03	AJ004862.1	NT	wc37c09.x1 NC1_CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3'
10780	23304	36312	1.61	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
10830	23448		1.68	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12273	25095		1.83	7.0E-03	H84085.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12281	24484		1.58	7.0E-03	BE263253.1	EST_HUMAN	Sporobolus stipticus mRNA for putative glycine and proline-rich protein
12382	24549		1.88	7.0E-03	Y17455.1	NT	yy15h01.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12527	25082		1.38	7.0E-03	AL183300.2	NT	Alu repetitive element
12684	24734		3.16	7.0E-03	AW888110.1	EST_HUMAN	601145154F2 NIH_MGC, 19 Homo sapiens cDNA clone IMAGE:3160476 5'
1283	13879	28400	10.8	8.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
1283	13879	28401	10.8	8.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G100
2800	16352	27821	1.82	8.0E-03	AF112374.1	NT	RCD-SN0032-110400-021-e04 SN0032 Homo sapiens cDNA
2916	15533	28004	3.54	8.0E-03	AA759135.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2916	15533	28005	3.54	8.0E-03	AA759135.1	EST_HUMAN	SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PYR;
3283	15894		2.17	8.0E-03	H76890.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
							SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PYR;
							Danio rerio odorant receptor gene cluster
							ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							yy77h04.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3344	15854		0.79	6.0E-03	AF180338.1	NT	Notocarus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3429	16037	28518	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vesolochin genes, complete cds
3429	16037	28519	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vesolochin genes, complete cds
3600	16204		1.13	6.0E-03	W37985.1	EST_HUMAN	zc13a1.1.1 Soares parathyroid tumor NB-HPA Homo sapiens cDNA clone IMAGE:322172 5'
3721	16322	28789	2.6	6.0E-03	BF510888.1	EST_HUMAN	UHH-B14-epm-c06-D.U1.s1 NCJ CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3757	16358	28828	1.53	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0606-200-400-014-s07 BT0606 Homo sapiens cDNA
3845	16444	28905	1.14	6.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA
3865	16583	28968	0.83	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240888-021-b10 CT0204 Homo sapiens cDNA
4030	16628		0.92	6.0E-03	BE250108.1	EST_HUMAN	600842804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858513 5'
4419	17004		1.1	6.0E-03	N58848.1	EST_HUMAN	Y62H10.s1 Soares multiple sclerosis 2NB-IMSP Homo sapiens cDNA clone IMAGE:278178 3'
4454	17040		1.58	6.0E-03	A1016833.1	EST_HUMAN	o3c11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4805	17383	28833	8.21	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5280	17832		0.92	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
6301	24761	31680	0.72	6.0E-03	9827521	NT	Varicella virus, complete genome
6808	18840	32478	0.73	6.0E-03	O14984	SWISSPROT	SYNAPSIN III
6839	18047	30469	0.72	6.0E-03	BE253748.1	EST_HUMAN	60111233F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3363172 5'
7642	20154	33040	0.78	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7774	20283	33180	24.22	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7799	20342	33251	6.91	6.0E-03	A1033990.1	EST_HUMAN	aw13604.x1 Soares parathyroid tumor NB-HPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
7915	20457	33363	2.45	6.0E-03	AW798337.1	EST_HUMAN	RCO-UM0051-210900-032-g02 UM0051 Homo sapiens cDNA
7980	20532		1.59	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858626 5'
9473	21872	34821	8.46	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9958	22451		2.15	6.0E-03	AJ432661.1	EST_HUMAN	822c02.x1 NCJ CGAP K14F11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10067	22582	35557	0.73	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ;
10197	22692		0.91	6.0E-03	AF084555.1	NT	Bacillus subtilis fmd gene
10303	22797	35788	0.63	6.0E-03	X68388.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10623	23155	36168	2.04	6.0E-03	AW982184.1	EST_HUMAN	M thermophilum complete plasmid pFV1 DNA
10890	23220		2.23	6.0E-03	11545814	NT	EST374237 MAGG resequences, MAGG Homo sapiens cDNA
							Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10728	23252	362089	2.16	6.0E-03	AI420786.1	EST_HUMAN	ts81c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
10728	23252	36270	2.16	6.0E-03	AI420786.1	EST_HUMAN	ts81c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
10881	23382		2.08	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10882	23383	36401	2.4	6.0E-03	BE737865.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
11630	24072	37134	1.57	6.0E-03	H70298.1	EST_HUMAN	yr95f01.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:6PGD_PIG P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ;
11828	24195		3.52	6.0E-03	AF010486.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
11856	24848		5.1	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 428192 to 450298 (section 39 of 148) of the complete genome
12038	24814		3.02	6.0E-03	U30780.1	NT	Pneumocystis carinii f. sp. reitii guanine nucleotide binding protein alpha subunit (pgc1) gene, complete cds
12088	24357		1.81	6.0E-03	Q62209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12402	24581		1.49	6.0E-03	BE788019.1	EST_HUMAN	601482821F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
12418	24571		1.52	6.0E-03	AJ245480.1	NT	Brassica napus sgl gene for S-locus glycoprotein, cultivar T2
12556	24942		1.6	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
229	12889	25375	5.16	5.0E-03	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
687	13320	25806	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
687	13320	25807	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
688	13320	25808	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
688	13320	25807	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
1151	13754	28264	0.91	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2706	15263	27830	2.77	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2982	15578	28057	0.88	5.0E-03	BE268057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538769 5'
3170	15784	28256	4.54	5.0E-03	T87823.1	EST_HUMAN	yc81f09.s1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:22385 3'
3188	15801		2.22	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3202	15814	28289	1.15	5.0E-03	IR17194.1	EST_HUMAN	y98g02.s1 Scores breast ZNHBst Homo sapiens cDNA clone IMAGE:155668 3'
3316	15828		0.88	5.0E-03	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3728	16328	28785	5.04	5.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3762	16303	28831	4.88	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3822	16422	28884	0.68	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4043	16841		1.78	5.0E-03	AA290875.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4204	16793	29239	0.57	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4392	16978	29425	0.88	5.0E-03	H78355.1	EST_HUMAN	y478g10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240088 5'
4394	16422	28884	0.71	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4670	17252	29704	0.68	5.0E-03	U46691.1	NT	Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds
4714	17295	29739	0.8	5.0E-03	AJ131016.1	NT	Homo sapiens SGL gene locus
4828	17406	29860	1.72	5.0E-03	A1752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5067	17840	30083	1.02	5.0E-03	P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5391	17949	30362	0.95	5.0E-03	AF171688.1	NT	Bos taurus acidic alpha-glucosidase gene, exons 2 through 20 and complete cds
5564	18598	31320	7.68	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6195	18805	31574	2.33	5.0E-03	Q00507	SWISSPROT	Chlamydia pneumoniae AR39, section 62 of 94 of the complete genome
6230	18838		0.91	5.0E-03	AE002234.2	NT	600944504T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880871 3'
6708	18302		10.88	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6832	18040	30483	6.39	5.0E-03	AB025024.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7106	18446		0.85	5.0E-03	AB038267.1	NT	RC3-CT0255-031099-011-407 CT0255 Homo sapiens cDNA
7595	20109		1.16	5.0E-03	AW854327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
7744	20252	33146	7.43	5.0E-03	AB016816.1	NT	RC8-CT0281-081198-011-A05 CT0281 Homo sapiens cDNA
8162	20703	33618	1	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081198-011-A05 CT0281 Homo sapiens cDNA
8162	20703	33618	1	5.0E-03	AW855907.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8181	20722	33636	2.28	5.0E-03	P46862	SWISSPROT	Mouse complement receptor (CR2) mRNA, 3' end
8548	21087		6.36	5.0E-03	M61132.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
8742	21281	34204	1.47	5.0E-03	D90723.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
8870	21408	34333	0.69	5.0E-03	M25090.1	NT	SOF1 PROTEIN
9503	22003	34960	0.45	5.0E-03	P33750	SWISSPROT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9753	22251	35254	0.82	5.0E-03	L21710.1	NT	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
9861	22378	35354	0.77	5.0E-03	AW821888.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10062	22557	35552	0.49	5.0E-03	AA533143.1	EST_HUMAN	h46h10.s1 NCI_CGAP_P9 Homo sapiens cDNA clone IMAGE:985587

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10238	22731	35722	0.92	5.0E-03	7882557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10599	23133		10.33	5.0E-03	T10598.1	EST_HUMAN	6894F Heart Homo sapiens cDNA clone 894
10831	23183	36175	2.28	5.0E-03	D28273.1	NT	Unknown nitrogen-fixing bacteria nifD gene encoding alpha subunit of dinitrogenase (MoFe protein)
10819	23340	36355	2.94	5.0E-03	AW170334.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
10820	23439	36460	2.02	5.0E-03	T49183.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
11212	23715		3.91	5.0E-03	BE048055.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
11972	25054		8.12	5.0E-03	AF047874.1	NT	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
12111	24372		21.73	5.0E-03	AF087263.1	NT	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
12217	24440		1.81	5.0E-03	L10347.1	NT	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
12250	24461		1.78	5.0E-03	AA456597.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
12283	24558		5.46	5.0E-03	BF572332.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
12473	24598	30883	2.21	5.0E-03	AW449109.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
12498	24932		1.42	5.0E-03	Q02388	SWISSPROT	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
253	12913	25387	2.58	4.0E-03	AW500196.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
343	12965	25480	1.77	4.0E-03	R49482.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
468	13101	25594	0.89	4.0E-03	P54675	SWISSPROT	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
629	13258	25730	3.12	4.0E-03	AA938339.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
910	13323	26043	1.75	4.0E-03	R49482.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
944	13557		3.19	4.0E-03	AW749101.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
1180	13781	26302	25.91	4.0E-03	AA088777.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
1211	13811	26325	1.71	4.0E-03	AW784740.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
1346	13941	26463	1.4	4.0E-03	AA284374.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
1630	14222		1.06	4.0E-03	AV708305.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
1770	14369	26913	2.74	4.0E-03	U33472.1	NT	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
2062	14842	27217	14.12	4.0E-03	AA088777.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
2289	14863		1.92	4.0E-03	BE410556.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
2317	14889	27484	2.83	4.0E-03	AW784740.1	EST_HUMAN	xt50g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15170	27737	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2608	15170	27738	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2715	15272	27838	3.14	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing G14ORF4 gene
2715	15272	27839	3.14	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing G14ORF4 gene
2721	15277	27842	1.25	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3262	15874	28355	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3262	15874	28356	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3583	16187	28689	0.85	4.0E-03	AW188426.1	EST_HUMAN	x88804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3583	16187	28670	0.85	4.0E-03	AW188426.1	EST_HUMAN	x88804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3685	16286	28755	0.63	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3698	16287	28767	0.63	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLC202 3'
4067	16863		1.83	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exon 1-11 (and joined CDS)
4323	16808	28350	1.88	4.0E-03	AI786727.1	EST_HUMAN	w87408.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2400274 3'
5307	17889	30291	2.1	4.0E-03	AW103719.1	EST_HUMAN	x863403.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2814469 3' similar to contains L1.11 L1
5354	17814	30329	1.17	4.0E-03	AA686895.1	EST_HUMAN	L1 repetitive element:
6433	17889	30395	1.19	4.0E-03	AL163284.2	NT	z88601.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:438009 3'
5480	18114	30523	1.36	4.0E-03	AF005858.1	NT	Homo sapiens chromosome 21 segment HS21C084
5588	18226	30873	21.16	4.0E-03	AF168825.1	NT	Drosophila melanogaster anon207 (anon207) mRNA, complete cds
5983	18585	31310	3.31	4.0E-03	P04186	SWISSPROT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5985	18587	31321	1.56	4.0E-03	P21849	SWISSPROT	(HPRG)
6042	18661	31400	0.97	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELLED TROPHOBLAST ANTIGEN PRECURSOR
6235	18844		3.41	4.0E-03	U22180.1	NT	DKF7p7811014.1 781 (synonym: hamy2) Homo sapiens cDNA clone DKF7p7811014 5'
6381	18985	31765	0.98	4.0E-03	AW590572.1	EST_HUMAN	Rattus norvegicus opsin gene, complete cds
6451	19052	31837	1.96	4.0E-03	BE548453.1	EST_HUMAN	hg46c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2848652 3'
6775	19367	32178	1.04	4.0E-03	AA813222.1	EST_HUMAN	601076010F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6872	19808	32440	1.51	4.0E-03	U78408.1	NT	ap32f11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1982045 3'
7130	19470	32288	1.13	4.0E-03	AL163278.2	NT	Lycopodium obscurum knotted 3 protein (TKN3) mRNA, complete cds
7130	19470	32289	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7249	19778	32633	6.46	4.0E-03	Q02817	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
							MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7459	19882	32847	1.14	4.0E-03	AI681483.1	EST_HUMAN	bc37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7461	19884	32849	0.95	4.0E-03	BE670170.1	EST_HUMAN	7e31b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7883	20425	33334	0.83	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
7882	20534	33438	4.22	4.0E-03	AF111944.1	NT	ADAMTS-5 (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8145	20688	33568	1.94	4.0E-03	7682087	NT	Dicystallum discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8648	21187	34105	8.89	4.0E-03	AI553983.1	EST_HUMAN	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8821	21360		4.46	4.0E-03	AL163209.2	NT	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
8830	21369	34293	3.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C008
9840	22338	35319	0.78	4.0E-03	H30864.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
10278	22773	35782	0.7	4.0E-03	AL161555.2	NT	yp42g12.1 Soares retina N2b5fR Homo sapiens cDNA clone IMAGE:190150 5'
11008	23523	36557	6.06	4.0E-03	AL163209.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11393	23845	36809	1.69	4.0E-03	AL208703.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
11393	23846	36910	1.69	4.0E-03	AL208703.1	EST_HUMAN	qp56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11807	24050	37118	1.82	4.0E-03	AE002102.1	NT	qp56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11838	25071		10.45	4.0E-03	BE915173.1	EST_HUMAN	Ureaplasma urealyticum section 3 of 59 of the complete genome
11862	24284		1.62	4.0E-03	BE298290.1	EST_HUMAN	PMA-BN0138-180800-002-b08 BN0138 Homo sapiens cDNA
12047	24331		2.71	4.0E-03	AW504273.1	EST_HUMAN	801118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12294	24493		3.88	4.0E-03	BF224125.1	EST_HUMAN	UL-HF-BND-4p-g-04-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12341	24975		2.24	4.0E-03	AW614598.1	EST_HUMAN	7q74c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12352	24532		3.01	4.0E-03	AW819141.1	EST_HUMAN	HN02c07.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
394	13040	25531	1.73	3.0E-03	AF011920.1	NT	RC3-ST0281-240400-015-f03 S10281 Homo sapiens cDNA
812	13525	26044	5.57	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1701	14294	26829	2.85	3.0E-03	AA468110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2288	14871		1.78	3.0E-03	AF055088.1	NT	nc73c05.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2333	14904		4.14	3.0E-03	Z32521.1	NT	Homo sapiens MHC class 1 region
2334	14905	27476	1.03	3.0E-03	U46858.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2334	14905	27476	1.03	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2448	15015	27587	1.13	3.0E-03	AF240786.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3022	15638		0.66	3.0E-03	Y08006.1	NT	Arabidopsis thaliana rpoMt gene
3119	15733	28203	3.26	3.0E-03	BE379298.1	EST_HUMAN	601237882F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3009933 5'
3186	15798	28270	3.21	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3464	16071	28544	2.13	3.0E-03	U34608.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3473	16079		7.31	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4049	16846	28114	7.57	3.0E-03	AV762382.1	EST_HUMAN	AV762382 MDS Homo sapiens cDNA clone MDSBSG01 5'
4049	16846	28115	7.57	3.0E-03	AV762382.1	EST_HUMAN	AV762382 MDS Homo sapiens cDNA clone MDSBSG01 5'
4109	16703	28156	1.75	3.0E-03	AI792278.1	EST_HUMAN	af04f09.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155889 5'
4485	17070	28520	6.2	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4580	17143		0.71	3.0E-03	BE348739.1	EST_HUMAN	h88g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151834 3'
4616	17169	28647	5.79	3.0E-03	AI538141.1	EST_HUMAN	ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4680	17535	28977	2.45	3.0E-03	AI732754.1	EST_HUMAN	601482719F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
4978	17553	28996	6.1	3.0E-03	BE787945.1	EST_HUMAN	Oryctolagus Cuniculus sod gene
5089	17642	30084	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus Cuniculus sod gene
5089	17642	30085	1.01	3.0E-03	AJ007044.1	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5470	18104	30423	3.56	3.0E-03	8822498	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18370	31078	1.18	3.0E-03	AJ248981.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
5809	18434	31155	13.97	3.0E-03	U35323.1	NT	aat13f10.r1 Soares_NIH-MIPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
6670	19268	32070	10.41	3.0E-03	AA456701.1	EST_HUMAN	Karyeromyces marianus pop3 gene for putative-cytosine permesase
7256	19784	32640	1.45	3.0E-03	AJ011418.1	NT	Oryza sativa gene for bZIP protein, complete cds
7531	20051	32824	3.37	3.0E-03	AB021736.1	NT	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7879	20421	33329	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7879	20421	33330	0.91	3.0E-03	BF333058.1	EST_HUMAN	z627604.s1 Soares_papillary tumor_NHPPA Homo sapiens cDNA clone IMAGE:304783 3'
8097	20638	33549	4.71	3.0E-03	N82580.1	EST_HUMAN	S.cerevisiae UGA35 gene, complete cds
8257	20788		0.55	3.0E-03	M63498.1	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8397	20837	33860	1.11	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS21C088
8419	20859	33877	1.31	3.0E-03	AL163268.2	NT	NONSTRUCTURAL PROTEIN V
8522	21061		1.37	3.0E-03	O8QM81	SWISSPROT	h88f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2889131 3' similar to contains L1.1 L1 repetitive element
8922	21460		12.62	3.0E-03	AW813774.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
8975	21513	34436	4.44	3.0E-03	AL161589.2	NT	

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8969	21536	34486	5.98	3.0E-03	A018731.1	EST_HUMAN	0403412x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:57138_mai
9008	21545	34474	0.82	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9030	21844		1	3.0E-03	D00001.1	NT	602035980F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4183638 5'
9068	20307	33210	0.86	3.0E-03	BE154670.1	EST_HUMAN	Synchocystis sp. PCC8803 complete genome, 3/27, 271600-402289
9554	22054		0.87	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071289-003-407 HT0344 Homo sapiens cDNA
9823	22123		5.92	3.0E-03	P08672	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPOROITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]
9809	22307	35291	1.98	3.0E-03	P11369	SWISSPROT	
9907	22404	35379	1.3	3.0E-03	P51889	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10048	22541	35538	3.96	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10728	23254		4.26	3.0E-03	5903028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11257	23787	36843	2.21	3.0E-03	AF008222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11321	23019	36028	1.99	3.0E-03	AF266285.1	NT	Homo sapiens goggin-like protein (GLP) gene, complete cds
11354	23808	36887	3.96	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11354	23808	36888	3.96	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11707	24869		2.32	3.0E-03	AI525056.1	EST_HUMAN	prmtm-5.E07.1 bruntar Homo sapiens cDNA 5'
							cd77b10.s1 Soares_tetis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to
							contains L1.13 MER26 repetitive element;
11743	24142	36763	1.31	3.0E-03	AA863154.1	EST_HUMAN	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
11804	25007		1.81	3.0E-03	AB009688.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
11898	24268	30884	2.67	3.0E-03	AJ286282.1	NT	
541	13172	25661	0.8	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
541	13172	25662	0.8	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
818	15426		11.05	2.0E-03	T70874.1	EST_HUMAN	Yd15K03.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1407	14000	26529	2.25	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1410	14003	26531	1.35	2.0E-03	AA661805.1	EST_HUMAN	nu8801.s1 NCI_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217563
1418	14011	26540	20.98	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
							PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN
							SFA-1) (CD151 ANTIGEN)
1526	14128	26684	1.04	2.0E-03	P48509	SWISSPROT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
							type VI) (PLOD) mRNA
1563	14155	26686	2.05	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1563	14155	26687	2.05	2.0E-03	4557836	NT	type VI) (PLOD) mRNA
1635	14277		5.58	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR

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1807	14397	26942	1.01	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1 Soares total_fetus Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1922	14507		0.89	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-061089-018-d03 HT0183 Homo sapiens cDNA
2038	14620	27188	1.25	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2291	14885	27440	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2815	15177		4.13	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adi-g-10-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3463	16070	28543	4.95	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1 Soares total_fetus Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3470	16076	28549	0.76	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3729	16330	28798	6.87	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
4024	16622	28084	0.89	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4191	16780	29228	2.48	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52, COAT PROTEIN GP36]
4302	16888		12.85	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4502	17088		1.08	2.0E-03	L35078.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4518	17102		1.34	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-ar-g-03-0-UI.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4523	17107	29553	0.96	2.0E-03	AI084746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4844	17228	29680	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shorttailed class 2 (shc) mRNA, complete cds
4844	17228	29681	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shorttailed class 2 (shc) mRNA, complete cds
4821	17399		1.92	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b-4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4848	17426	29878	5.2	2.0E-03	AA908488.1	EST_HUMAN	d14R05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1523457 3'
5167	17738	30163	0.81	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5428	17885		0.9	2.0E-03	AF205067.1	NT	Desulfovibrio desulfuricans cytochrome c3 precursor (cycA) gene, complete cds
5678	18305	30787	1.16	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104892 5'
5810	24749	31158	2.28	2.0E-03	AB014583.1	NT	Homo sapiens mRNA for KIAA0683 protein, partial cds
5887	18510	31238	2.11	2.0E-03	U63711.1	NT	Xenopus laevis xellin mRNA, complete cds
6258	18967	31636	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6258	18967	31637	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6488	19087	31889	2.38	2.0E-03	Q96203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6488	19087	31870	2.38	2.0E-03	Q96203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6488	19089	31972	7	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19121	31912	2.17	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAM-TS7)
6546	19144	31940	1.46	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)

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6715	19309		2.03	2.0E-03	AB991089.1	EST_HUMAN	wu36109.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW RL28_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 :contains element MSR1 repetitive element :
7038	18058	30480	0.99	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7104	19874	32513	1.54	2.0E-03	5031884	NT	Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA
7104	19874	32514	1.54	2.0E-03	5031884	NT	Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA
7141	19521	32343	3.59	2.0E-03	BE067988.1	EST_HUMAN	CMA-BT0368-081290-054-d01 BT0368 Homo sapiens cDNA
7198	19729	32590	0.7	2.0E-03	AI298883.1	EST_HUMAN	qim9d11.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7335	19882	32726	0.87	2.0E-03	T86569.1	EST_HUMAN	yd77g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7613	20128	33003	1.49	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN)(LP)
7695	20537	33440	2.47	2.0E-03	AW582004.1	EST_HUMAN	m37608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60978
8159	20700	33614	5.98	2.0E-03	N20287.1	EST_HUMAN	Q60978.JERKY. ; yk42g08.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element ;
8159	20700	33615	5.98	2.0E-03	N20287.1	EST_HUMAN	yk42g08.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element ;
8208	20749	33682	0.52	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN O8G9.05 IN CHROMOSOME 1
8228	20789	33688	0.94	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8282	20823	33743	0.82	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8282	20823	33744	0.82	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8307	20848	33771	0.8	2.0E-03	AU136678.1	EST_HUMAN	AU136678 PLACE1 Homo sapiens cDNA clone IMAGE:1004638 5'
8358	20898		2.04	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8123	18508	31253	0.89	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-02 UM0025 Homo sapiens cDNA
8123	18508	31254	0.89	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-02 UM0025 Homo sapiens cDNA
9164	21699	34843	0.85	2.0E-03	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9445	21871	34820	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:184296 3'
9445	21871	34821	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:184296 3'
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GNEM) (J1) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9477	21876	34823	2.57	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35049	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35050	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9639	22139	35105	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9639	22139	35106	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9828	22327	35308	0.98	2.0E-03	AW884289.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
9856	22460		4.55	2.0E-03	AA261376.1	EST_HUMAN	zs10a08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
10894	23415		3.24	2.0E-03	M88524.1	NT	Human dystrophin gene
11361	20126	33003	2.13	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11417	23889		2.26	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11424	23875	36939	13.97	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
11687	24103		3.17	2.0E-03	AK25745.1	EST_HUMAN	Y65H03.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW-VATG_MANSE
11705	24119	37151	4.77	2.0E-03	AF157519.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
11730	24135	37155	1.94	2.0E-03	A084325.1	EST_HUMAN	oy43g08.s1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to
11754	18032		8.96	2.0E-03	AJ245167.1	NT	TR:P97535 P97535 PS-PLA1 PRECURSOR.;
11907	25050		2.34	2.0E-03	AV697866.1	EST_HUMAN	Carneius dromedarius chrp19 gene for immunoglobulin heavy chain variable region
12062	24345	30984	1.49	2.0E-03	Y00508.1	NT	AV697866 GKG Homo sapiens cDNA clone GKGX005 5'
							H. sapiens M1 gene for muscarinic acetylcholine receptor
12372	24542		2.06	2.0E-03	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12551	24849		5.07	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKG Homo sapiens cDNA clone GKGX005 5'
494	13098	25599	1.93	1.0E-03	H98471.1	EST_HUMAN	Y68c08.r1 Soares_pneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
							as70b08.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
862	13477	25902	1.47	1.0E-03	A1720283.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOVYL-COA HYDRATASE.;
							as70b08.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
862	13477	25903	1.47	1.0E-03	A1720283.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOVYL-COA HYDRATASE.;
1134	13737	26246	2.21	1.0E-03	A1865788.1	EST_HUMAN	w486a08.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1154	13757	26267	1.31	1.0E-03	A1854572.1	EST_HUMAN	w483e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
							w486a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
1208	13808	26321	1.67	1.0E-03	A1692616.1	EST_HUMAN	
2074	14654	27227	4.05	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMYMI)
2189	14775	27348	9.98	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3008	15624	28102	1.45	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
							CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED
3225	15837	28315	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

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3225	18637	28316	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3341	15951	28427	0.79	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3598	18200	28683	0.65	1.0E-03	U68081.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3598	18200	28684	0.65	1.0E-03	U68081.1	NT	Human MUC2 gene, promoter region
3727	18328		1.31	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
3997	16595	28087	0.75	1.0E-03	AW170532.1	EST_HUMAN	Human sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4008	16606	28080	0.81	1.0E-03	Z46849.1	NT	xr63d07.x1 Soares_NHCC cervical tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to
4528	17112	28656	4.29	1.0E-03	BE930162.1	EST_HUMAN	contains TAR1.11 TAR1 repetitive element;
4574	17157	28801	5.77	1.0E-03	BE246538.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR148w
4770	17351	28803	0.83	1.0E-03	U28449.1	NT	RC1-TN0128-180800-021-g01 TN0128 Homo sapiens cDNA
4850	17525	28888	2.83	1.0E-03	A073485.1	EST_HUMAN	TCBAP1D4809 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP-4809
4850	17525	28887	2.83	1.0E-03	A073485.1	EST_HUMAN	Casorhabdilis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4851	17528		5.92	1.0E-03	BE154087.1	EST_HUMAN	ow45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
5236	17800	30219	11.45	1.0E-03	Q48408	SWISSPROT	ow45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
5511	18144	30556	2.02	1.0E-03	AA280951.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5598	18228	30878	2.74	1.0E-03	AJ008345.1	NT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5847	18275	30749	1.7	1.0E-03	K03332.1	NT	zs44f01.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5847	18275	30750	1.7	1.0E-03	K03332.1	NT	Homo sapiens KVLQ11 gene
5761	18387	31101	0.92	1.0E-03	BE708491.1	EST_HUMAN	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5766	18392	31105	1.72	1.0E-03	Q02388	SWISSPROT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
6171	18783		2.62	1.0E-03	X07699.1	NT	80158841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943854 5'
6209	18819	31580	1.1	1.0E-03	BE983839.2	EST_HUMAN	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
6339	18945		8.29	1.0E-03	11528178	NT	Mouse nucleolin gene
6476	19077	31860	1.21	1.0E-03	T87761.1	EST_HUMAN	801657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6541	19140		1.4	1.0E-03	AW002585.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6852	19441	32258	1.31	1.0E-03	L77570.1	NT	y483a1.1.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115772 5'
7206	19737	32580	2.48	1.0E-03	D16828.1	NT	QV3-NN1024-280400-171-g05 NN1024 Homo sapiens cDNA
7468	20021		1.72	1.0E-03	AJ28042.1	NT	Homo sapiens DGGeorge syndrome critical region, centromeric end
						NT	Human gene for fourth somatostatin receptor subtype
						NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
						NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7635	20147	33030	1.7	1.0E-03	U52111.2	NT	

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7604	20203	33080	3.21	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7734	20242	33133	1.13	1.0E-03	BE88044.1	EST_HUMAN	601461061F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
7830	20372	33279	0.57	1.0E-03	AF274591.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7891	20433	33342	6.79	1.0E-03	AJ261973.1	NT	Homo sapiens partial steerin-1 gene
8086	20627	33541	1.29	1.0E-03	AA122270.1	EST_HUMAN	z697c09.s1 Soares_pregnant_uterus_NH-IPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element;
8188	20727	33639	2.03	1.0E-03	AF153080.1	NT	Homo sapiens exocytosis-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8369	20908	33828	0.81	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca ²⁺ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8530	21069	33988	0.52	1.0E-03	AA001613.1	EST_HUMAN	z182608.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8530	21069	33989	0.52	1.0E-03	AA001613.1	EST_HUMAN	z182608.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8873	21412		1.29	1.0E-03	Y11204.1	NT	V. carteri gene encoding volvoxapain
8900	21438	34391	0.59	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0079-170200-092-07 LT0079 Homo sapiens cDNA
9008	21549		0.68	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca ²⁺ /calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9047	21594	34514	3.37	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cH1 subunit mRNA, complete cds
9047	21594	34515	3.37	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cH1 subunit mRNA, complete cds
9525	22025	34882	1.98	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9525	22025	34883	1.98	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9734	22232	35210	0.94	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG-40) (DERMATAN SULFATE)
10068	22583	35558	0.57	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10073	22598		0.75	1.0E-03	AF067485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10218	22713	35705	1.25	1.0E-03	AJ024350.1	EST_HUMAN	ov7508.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1943175 3' similar to contains MER39.b1
10545	23082	36095	1.71	1.0E-03	AW362393.1	EST_HUMAN	MER39 MER39 repetitive element;
10545	23082	36096	1.71	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
10628	23161	36173	3.2	1.0E-03	BE170859.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
							QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
							tt3612.x1 NCJ_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246448 3' similar to TR-Q26195 Q26195 PVA1 GENE.;
10703	23232		3.19	1.0E-03	AJ583847.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11036	23550		3.78	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone IMAGE:3918524 5'
11882	24099	37149	4.46	1.0E-03	BE880448.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12149	24392	30974	1.27	1.0E-03	9507208	NT	Rattus norvegicus transformation related protein 63 (Trp63), mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12175	25030		5.99	1.0E-03	A347355.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12282	25052	30510	5.72	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5862	18484		1.63	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6612	19209	32017	1.08	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9561	22061		1.56	9.0E-04	A8037203.1	NT	Glycylhistidyl transferase GbAS1 mRNA for beta-amylin synthase, complete cds
1535	14127		1.05	8.0E-04	X98468.1	NT	Xlaeids mRNA for CASR protein
4259	16945		5.17	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4880	17455	28808	2.55	8.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11024	23338		2.15	8.0E-04	AA77084.1	EST_HUMAN	z24c10.s1 Soares_fetal_hairt_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11175	23682		2.5	8.0E-04	A1571089.1	EST_HUMAN	in85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
12500	24626	30892	1.65	8.0E-04	AW578654.1	EST_HUMAN	PM2-HT0353-130100-002-110 HT0353 Homo sapiens cDNA
1867	14453	27012	0.99	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2442	16009	27681	0.92	7.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2739	15294	27861	1.75	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3319	15929	28406	1.23	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
6246	18555	31628	0.75	7.0E-04	AA518212.1	EST_HUMAN	ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:909718 similar to contains L1.b3 L1 L1 repetitive element;
6636	19232		2.63	7.0E-04	A1786331.1	EST_HUMAN	wg36f08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7279	19807		0.79	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ30035 protein, partial cds
9719	22217	35181	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9719	22217	35182	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11440	23890		3.42	7.0E-04	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11463	23913	36880	2.68	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12222	24443		11.57	7.0E-04	BE077941.1	EST_HUMAN	GM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
12472	24597		4.94	7.0E-04	R17338.1	EST_HUMAN	y813c08.l1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
12505	24628		7.97	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2720	15278		0.93	6.0E-04	BF341380.1	EST_HUMAN	502013338F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149287 5'
4033	16631	28100	1.61	6.0E-04	A882525.1	EST_HUMAN	wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4163	16754	29205	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4163	16754	29206	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4284	16850	29238	3.2	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4538	17122	28567	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-809 HT0560 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4538	17122	28508	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-180200-011-009 HT0560 Homo sapiens cDNA
5413	17970	30378	0.9	6.0E-04	A1806687.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
5413	17970	30380	0.9	6.0E-04	A1806687.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
7807	20350		3.04	6.0E-04	P46406	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7868	20500		0.67	6.0E-04	H92847.1	EST_HUMAN	y94c11.s1 Soares_pituitary_gland_N3-HPG Homo sapiens cDNA clone IMAGE:231856 3' similar to contains LOR1 repetitive element;
9890	22387		3.74	6.0E-04	AL046507.2	EST_HUMAN	DKFZp568M2024_r1 586 (synonym: hube1) Homo sapiens cDNA clone DKFZp568M2024
9924	22420		0.77	6.0E-04	A1858286.1	EST_HUMAN	w335p02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426830 3'
9862	22487	35475	2.18	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-H11 BN0120 Homo sapiens cDNA
10242	22737		0.64	6.0E-04	AF287478.1	NT	Lyttechinus variegatus embryonic blastocyst extracellular matrix protein precursor (ECM3) mRNA, complete cds
11358	23812	36872	2.9	6.0E-04	AJ228042.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11441	23891	36958	5.11	6.0E-04	AW013847.1	EST_HUMAN	ULH-B10-esb-0-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11495	23944	Q01768	2.28	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
11889	24828		3.55	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-281189-012-008 HT0269 Homo sapiens cDNA
12671	24739		1.01	6.0E-04	A1817088.1	EST_HUMAN	w178g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
679	13303	25785	8.64	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF82)
1549	14141		1.68	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021089-030-007 CT0225 Homo sapiens cDNA
3460	18087	28540	1.53	5.0E-04	AA548831.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3778	18378	28943	1.02	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5664	18281	30770	1.98	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6740	18334	32141	6.37	5.0E-04	AA156080.1	EST_HUMAN	2033p08.r1 Strabagene colon (#837204) Homo sapiens cDNA clone IMAGE:588863 5'
7411	18936	32801	16.91	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
7898	20440	33346	4.97	5.0E-04	A1188382.1	EST_HUMAN	q413f06.x1 Soares_placenta_8to9weeks_2Nbl-HP6b9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element
8245	20786	33705	0.91	5.0E-04	AA814519.1	EST_HUMAN	cb86602.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
8201	21718	34682	1.37	5.0E-04	AA846545.1	EST_HUMAN	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8283	21883	34840	0.8	5.0E-04	N83785.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9437	21883	34912	0.85	5.0E-04	P28128	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9527	22027	34988	4.43	5.0E-04	AW270938.1	EST_HUMAN	xs08e02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10855	23378		4.52	5.0E-04	AL048507.2	EST_HUMAN	DKFZp568M2024_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp568M2024
11559	18291	30770	11.05	5.0E-04	AF248054.1	NT	Bos taurus mitochondrial calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
11631	18838	32801	1.84	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
11809	24857		3.21	5.0E-04	AA588513.1	EST_HUMAN	nf18r02.s1 NCI CGAP_P71 Homo sapiens cDNA clone IMAGE:913875
12353	24883		1.77	5.0E-04	U83834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
415	13050		0.84	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
701	13323	.28810	1.12	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
880	13494	28012	1.46	4.0E-04	AI720283.1	EST_HUMAN	as70808.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
880	13494	28013	1.46	4.0E-04	AI720283.1	EST_HUMAN	Q13825 AL-BINDING PROTEINENYOYL-COA HYDRATASE. ;
1514	14108	28842	9.82	4.0E-04	AW763356.1	EST_HUMAN	as70808.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2130	14708	27280	1.59	4.0E-04	AL163278.2	NT	Q13825 AL-BINDING PROTEINENYOYL-COA HYDRATASE. ;
2179	14756		1.34	4.0E-04	AL048704.1	EST_HUMAN	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2656	15215	27787	1.83	4.0E-04	O98815	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
3200	15912	28288	2.59	4.0E-04	AF281074.1	NT	DKFZp434D059_l1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
3405	16014	28483	0.58	4.0E-04	AV886824.1	EST_HUMAN	SERICIN-2 (SILK GUM PROTEIN 2)
3935	16533		0.94	4.0E-04	AL163287.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4415	17000	28442	3.2	4.0E-04	AA576331.1	EST_HUMAN	AV886824 GK Homo sapiens cDNA clone GKCFH07 5'
4415	17000	28443	3.2	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C087
4635	17218	28671	1.94	4.0E-04	AA086324.1	EST_HUMAN	nh10a10.s1 NCI CGAP_Cor1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL
5249	17812	30235	6.04	4.0E-04	BE560860.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7312	18940	32899	1.25	4.0E-04	P48442	SWISSPROT	nh10a10.s1 NCI CGAP_Cor1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL
7541	20061		2.42	4.0E-04	AL161588.2	NT	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
8473	21013	33829	1.42	4.0E-04	BF240712.1	EST_HUMAN	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562870 3'
8481	21020	33835	1.85	4.0E-04	N25507.1	EST_HUMAN	60145885F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
							EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
							Arabisopsis thaliana DNA chromosome 4, contig fragment No. 86
							601875865F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089700 5'
							yc38a12.r1 Soares melanocyte 2NtHM Homo sapiens cDNA clone IMAGE:264142 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9608	22108	35070	2.79	4.0E-04	AI025699.1	EST_HUMAN	cr67r03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:184341 3'
9754	22252		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12180	24833		2.4	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
167	12830	25316	2.71	3.0E-04	AL119428.1	EST_HUMAN	DKFZp781J221.1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781J221 5'
209	12870	25356	3.63	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
913	13528	26045	1.72	3.0E-04	U83891.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1879	14485	27022	5.5	3.0E-04	AI282100.1	EST_HUMAN	qz28-d03.y1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2028197 5'
1894	14479		1.08	3.0E-04	AI389874.1	EST_HUMAN	h23a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3349	15858	28434	4.95	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
4038	16834	29103	3.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4131	16723		1.37	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4167	16758		1.14	3.0E-04	BE140608.1	EST_HUMAN	RC0-HT0014-310598-028 HT0014 Homo sapiens cDNA
4941	17516		5.05	3.0E-04	BE153778.1	EST_HUMAN	PM0-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
6162	17731	30158	0.57	3.0E-04	Q08472	SWISSPROT	E1A-ASSOCIATED PROTEIN P300
6282	18800		5.93	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6809	18588	32385	1.97	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7660	20105	32681	1.04	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8202	20743	33656	6.78	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9834	22332	35313	1.46	3.0E-04	AA454055.1	EST_HUMAN	zv48d08.l1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb-M62782
10080	22575	35570	0.5	3.0E-04	AB92139.1	EST_HUMAN	wk75a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513278 3'
							aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513278 3'
10358	22850	35844	8.78	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb-M36072 80S
							RIBOSOMAL PROTEIN L7A (HUMAN);
11758	25072	30514	3.55	3.0E-04	AA228301.1	EST_HUMAN	nc38a04.l1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010450 similar to contains L1.12 L1
12140	24909	30713	4.28	3.0E-04	AB018292.1	NT	repetitive element;
12574	24671		3.54	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
187	12848	25333	1.23	2.0E-04	AF217798.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
504	13136	25624	2.86	2.0E-04	AU146707.1	EST_HUMAN	DKFZp547L185.1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547L185 5'
940	13553	26088	5.4	2.0E-04	M86524.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
940	13553	26070	5.4	2.0E-04	M86524.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
							Human dystrophin gene
							Human dystrophin gene
1221	13821		3.94	2.0E-04	AI286021.1	EST_HUMAN	qh08a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	13827		1.95	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1872	14458		1.12	2.0E-04	AF224208.1	NT	Mus musculus 5' flanking region of Pib3 gene
2227	14802		0.9	2.0E-04	AA478880.1	EST_HUMAN	Z13805.x1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element
2610	15172	27740	6.83	2.0E-04	U68091.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBU1S1, TORBU1S2.>
3016	15832	28109	1.13	2.0E-04	AI124528.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539780 3'
3377	15886	28484	0.76	2.0E-04	6174738	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3483	16089	28561	2.53	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA
3983	16581	29052	0.85	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4224	16812		6.34	2.0E-04	U01026.1	NT	Phaeosolus vulgaris nitrate reductase (PNR2) gene, complete cds
4776	17357	28809	1.34	2.0E-04	H86285.1	EST_HUMAN	y01e11.1 Soares_pituitary_gland_N3H-PG Homo sapiens cDNA clone IMAGE:232558 5'
4776	17357	28810	1.34	2.0E-04	H86285.1	EST_HUMAN	y01e11.1 Soares_pituitary_gland_N3H-PG Homo sapiens cDNA clone IMAGE:232558 5'
4913	17488		1.79	2.0E-04	U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5215	17780	30189	1.44	2.0E-04	AB037697.1	NT	Danio rerio hagaromo gene, exons 1 to 6, partial cds
5733	18359	31085	1.82	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5745	18371	31079	1.87	2.0E-04	AI690862.1	EST_HUMAN	tq3b11.x1 NC1_CGAP_U3 Homo sapiens cDNA clone IMAGE:2207709 3'
5924	18548	31272	0.87	2.0E-04	AA296852.1	EST_HUMAN	EST111191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6102	18718	31470	1.06	2.0E-04	4758178	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6385	18889	31769	0.81	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7281	19809		2.44	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5'
7616	20129		13.08	2.0E-04	P08548	SW/ISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7826	20138	33017	1.26	2.0E-04	P64286	SW/ISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7897	20439	33344	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7897	20439	33345	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8226	20767	33685	0.97	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8226	20767	33686	0.97	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8500	21039	33680	1.77	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8678	21217	34137	0.56	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
8257	21783	34736	0.47	2.0E-04	AA725700.1	EST_HUMAN	af22a12.s1 Soares testis_NHT Homo sapiens cDNA clone 1343518 3'
9340	21854	34803	0.5	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLG28.1
8885	22382	35357	1.4	2.0E-04	BE149303.1	EST_HUMAN	RC3-HIT0254-151098-011-b05 HT0254 Homo sapiens cDNA
8930	22426	35400	2.39	2.0E-04	AA405777.1	EST_HUMAN	zu68c11.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742884 5'
10731	23257	36273	6.22	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11185	23680	36737	5.43	2.0E-04	AI440282.1	EST_HUMAN	001f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
11303	23786	36854	2.72	2.0E-04	AW136740.1	EST_HUMAN	UIH-B11-adm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
789	13416	25920	1.41	1.0E-04	H89848.1	EST_HUMAN	y226c09.s1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:282884 3' similar to contains L1.1 L1 repetitive element
1113	13717	26227	2.57	1.0E-04	P11368	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1153	13766	26266	4.04	1.0E-04	AW013947.1	EST_HUMAN	UIH-B10-eab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1153	13766	26266	4.04	1.0E-04	AW013947.1	EST_HUMAN	UIH-B10-eab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1377	13970		3.95	1.0E-04	U82918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1698	14282	26795	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1698	14282	26795	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1901	14486	27047	2.44	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
2711	15288	27835	1.09	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
2711	15288	27836	1.09	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
3323	15933	28410	1.1	1.0E-04	Q82203	SWISSPROT	SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3789	16399	28864	2.7	1.0E-04	AI440282.1	EST_HUMAN	001f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
4134	16726	29180	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4158	16748	29201	1.27	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBBD04 3'
5263	17825	30250	0.95	1.0E-04	AI357156.1	EST_HUMAN	q82h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
6021	18840	31380	1.5	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6568	19166	31902	0.97	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:252

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6825	19584	32414	0.78	1.0E-04	AA584561.1	EST_HUMAN	in25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:883488 3' similar to gb:M97252
7237	19767	32823	14.08	1.0E-04	AL251880.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7572	19767	32823	14.23	1.0E-04	AL251880.1	EST_HUMAN	q157d10.x1 NCI_CGAP_OV32 Homo sapiens cDNA clone IMAGE:1985683 3'
7837	20478	33389	1.02	1.0E-04	AA630453.1	EST_HUMAN	q157d10.x1 NCI_CGAP_OV32 Homo sapiens cDNA clone IMAGE:1985683 3'
8280	21788	34738	2.34	1.0E-04	AB06220.1	EST_HUMAN	ab94g08.s1 Stratiogene lung (H937210) Homo sapiens cDNA clone IMAGE:854654 3'
9270	21798	34745	1.71	1.0E-04	O88068	SWISSPROT	wf26c08.x1 Scores_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9346	21880		0.78	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9594	22084	35023	2.2	1.0E-04	10963978	NT	y472c08.l1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:113774 5'
10081	22578		2.87	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10116	22811	35601	0.83	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11218	23721		2.06	1.0E-04	M26567.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11503	23852	37020	1.98	1.0E-04	AB032688.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11540	23888	37050	2.1	1.0E-04	AW269081.1	EST_HUMAN	Homo sapiens mRNA for KIAA1142 protein, partial cds
11570	24017	37086	1.87	1.0E-04	Q39698	SWISSPROT	xx49g12.x1 Scores_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11570	24017	37087	1.87	1.0E-04	Q39698	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11670	24082		1.57	1.0E-04	BE886768.1	EST_HUMAN	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11919	24878		1.99	1.0E-04	BE876388.1	EST_HUMAN	CM4-CT0404-130700-476-H03 CT0404 Homo sapiens cDNA
727	13347	25839	1.98	9.0E-05	AA718833.1	EST_HUMAN	712a10.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:326058 3' similar to contains L1.13 L1
2047	14629	27198	0.92	9.0E-05	AW868218.1	EST_HUMAN	repetitive element;
8117	18733	31486	1.45	9.0E-05	Q80716	SWISSPROT	at45c11.s1 Scores_beslie_NHT Homo sapiens cDNA clone 1292468 3'
9397	21820		2.71	9.0E-05	D85606.1	NT	QV4-SN0023-070400-168-H04 SN0023 Homo sapiens cDNA
9399	21822	34771	2.79	9.0E-05	AF120882.1	NT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11017	23531	36567	2.86	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
11121	23629	36671	1.99	9.0E-05	A297878.1	EST_HUMAN	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11483	18733	31486	3.89	9.0E-05	Q80716	SWISSPROT	xs34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
							repetitive element;
							q123f08.x1 NCI_CGAP_Lyn8 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
							MIR repetitive element;
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11974	24939		4.26	9.0E-05	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1; DD4H, G8b, G8c, G8d, G8e, G8f, BAT5, G9b,
854	13470	25681	1.21	8.0E-05	AJ251648.1	NT	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
897	13511		9.89	8.0E-05	AJ251648.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gms2 gene)
							Pisum sativum mRNA for beta-1,3 glucanase (gms2 gene)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2677	15583		0.71	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4579	17162	29604	1.87	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8883	21222	34142	0.49	8.0E-05	Y11686.1	NT	Mus musculus gene for hexokinase II, exon 1 (end joined CDS)
11030	23544	36591	2.32	8.0E-05	M89197.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
12613	24621		2.72	8.0E-05	AA278333.1	EST_HUMAN	z888h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704583 3' similar to contains Alu repetitive element contains element MSR1 repetitive element ;
369	13018	25501	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
369	13018	25502	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA
593	13223	25697	3.82	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
593	13223	25698	3.82	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
1063	13698	26208	1.41	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2744	15266	27865	3.67	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3194	15808	28279	4.69	7.0E-05	AB009080.1	NT	Dicyostelium discoideum gene for TRFA, complete cds
4462	17048	29492	1.73	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4543	17127	29570	0.58	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
8167	20708	33624	1.11	7.0E-05	AA505582.1	EST_HUMAN	nh93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966098 3'
9472	21871	34820	3.74	7.0E-05	T07065.1	EST_HUMAN	EST04984 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBED80
11040	23554		7.95	7.0E-05	10835048	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2073	14653	27225	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2073	14653	27226	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2624	15186	27753	1.34	6.0E-05	A1855241.1	EST_HUMAN	w654h08.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2709	15268	27833	0.9	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28810
2709	15268	27834	0.9	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28810
2840	13328	25815	2.88	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5352	17912	30327	1.3	6.0E-05	AW962309.1	EST_HUMAN	EST174382 MAGE resequences, MAGG Homo sapiens cDNA
6071	18698	31432	3.12	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6071	18698	31433	3.12	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6535	19135	31928	1.45	6.0E-05	N72829.1	EST_HUMAN	yw50g11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246212 5'
7013	19511	32332	0.79	6.0E-05	AA897880.1	EST_HUMAN	q98a03.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8029	20571	33475	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-h08 BT0311 Homo sapiens cDNA
8029	20571	33476	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-h08 BT0311 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8381	20821	33841	0.85	6.0E-05	AA150482.1	EST_HUMAN	208c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491728 3' similar to contains element MER28 repetitive element;
8385	20825	33845	2.3	6.0E-05	AW886828.1	EST_HUMAN	PM4-NIN0050-310300-001-110 NIN0050 Homo sapiens cDNA
8516	21055	33978	0.62	6.0E-05	Q80401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9176	21753	34699	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9176	21753	34700	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9440	21988	34915	1.13	6.0E-05	T94149.1	EST_HUMAN	ye28c12.11 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:119082 5'
9637	22137	35103	0.57	6.0E-05	AW627895.1	EST_HUMAN	h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10627	23159	36172	3.98	6.0E-05	R75639.1	EST_HUMAN	ye6d08.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:119082 5' repetitive element; contains LTR7 repetitive element;
11394	23848	36911	4.18	6.0E-05	AA044015.1	EST_HUMAN	2k58f02.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12183	24919	30716	10.28	6.0E-05	AW890110.1	EST_HUMAN	MR0-NT0038-250400-001-409 NT0038 Homo sapiens cDNA
1449	14041	26569	18.37	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241189-040-111 ST0234 Homo sapiens cDNA
1903	14488		1.75	6.0E-05	8923691	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
4051	18048	29116	3.86	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLG22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5716	18342	30848	11.26	5.0E-05	X59855.1	NT	Human ML C1emb gene for embryonic myosin alkaline light chain, 3'UTR
6144	18758	31518	2.97	6.0E-05	AV863544.1	EST_HUMAN	AV863544 GLC Homo sapiens cDNA clone GLCMA08 3'
6316	18923	31700	0.97	5.0E-05	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7370	19698		1.22	5.0E-05	AB037984.1	NT	Mus musculus gene for calretinin, exon 1
11971	24460		5.73	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12248	24460		9.18	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2833	12906		3.49	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4580	17163	29605	1.37	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4580	17163	29608	1.37	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
5166	17735	30162	0.58	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7020	19518	32340	0.75	4.0E-05	U01947.1	NT	Macaca mulatta hemoglobin (HP) gene, 5' region
9442	21988		7.26	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]
9612	22408	35384	0.55	4.0E-05	P11369	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10305	22788	35790	0.73	4.0E-05	P23780	SWISSPROT	h38c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element;
10648	23180	36183	5.05	4.0E-05	AW627948.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
11850	24210	31041	3.27	4.0E-05	AL163252.2	NT	h38c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
11929	24264		1.38	4.0E-05	AW117590.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
709	13330	25817	0.64	3.0E-05	AI248061.1	EST_HUMAN	qf84c10.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1097	13702	26212	1.49	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1170	13772	26280	1.51	3.0E-05	BF037688.1	EST_HUMAN	601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3865142 5'
1170	13772	26281	1.51	3.0E-05	BF037688.1	EST_HUMAN	601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3865142 5'
2748	15301	27867	1.17	3.0E-05	Q62234	SWISSPROT	SKELEMIN
3331	15941		0.69	3.0E-05	AI288819.1	EST_HUMAN	qf91g11.x1 Scores_NHIMPJ_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4471	17057	28503	7.22	3.0E-05	BE168211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN ;
4471	17057	28504	7.22	3.0E-05	BE168211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4565	17148	28594	1.06	3.0E-05	AA368678.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4565	17148	28595	1.06	3.0E-05	AA368678.1	EST_HUMAN	EST178986 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4682	17274		0.71	3.0E-05	AL163302.2	NT	EST178986 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4728	17307	29751	0.75	3.0E-05	AF149773.1	NT	Homo sapiens chromosome 21 segment HS21C102
4963	13330	25817	0.65	3.0E-05	AI248061.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5748	18372	31080	1.73	3.0E-05	11072102	NT	qf84c10.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
6854	19442	32257	1.28	3.0E-05	AJ225782.1	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myo2pl), mRNA
6854	19442	32258	1.28	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7839	20381	33266	1.9	3.0E-05	BE733167.1	EST_HUMAN	Homo sapiens SYBL1 gene, exons 6-8
8283	20634	33756	1.28	3.0E-05	AA284049.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8824	21363	34288	1.78	3.0E-05	AW770982.1	EST_HUMAN	zs60605.s1 Stratiene echizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8828	21387	34291	1.22	3.0E-05	6912431	NT	h194608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
8832	21371	34286	0.47	3.0E-05	P43361	SWISSPROT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9058	21595		0.88	3.0E-05	X03273.1	NT	MELANOMA-ASSOCIATED ANTIGEN 8 (IMAGE-8 ANTIGEN)
9244	21770	34718	1.3	3.0E-05	AA372662.1	EST_HUMAN	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9581	22081		2.97	3.0E-05	AJ769331.1	EST_HUMAN	EST184475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
10428	22922	35925	0.85	3.0E-05	Q62818	SWISSPROT	wg36f09.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10428	22922	35926	0.85	3.0E-05	Q62818	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12055	24338		1.48	3.0E-05	AJ271735.1	NT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12387	25101		1.52	3.0E-05	AW518689.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
2362	14833	27508	1.55	2.0E-05	AI286021.1	EST_HUMAN	zs89408.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2776811 3'
2619	15181	27747	10.28	2.0E-05	M13792.1	NT	qf88e11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
							Human adenosine deaminase (ADA) gene, complete cds

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2738	15283		6.76	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.1 Stragene hNT neuron (#337233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3171	15785	28257	1.59	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3391	15889	28477	0.63	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3416	16024	28506	1.04	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3541	16146		0.72	2.0E-05	X95465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3880	16478		0.67	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5681084_r1 668 (synonym: hkd2) Homo sapiens cDNA clone DKFZp5681084 5'
5010	17583	30028	0.63	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5176	17743		2.42	2.0E-05	L77589.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5933	18555	31282	1.64	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6125	18740	31462	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUMDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6125	18740	31463	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUMDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6305	18912	31686	0.73	2.0E-05	A1148272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_86dweeks_2hbp89uW Homo sapiens cDNA clone IMAGE:1715114 3' similar to contains L1 L3 L1 repetitive element;
6736	19330	32136	2.12	2.0E-05	AA714330.1	EST_HUMAN	hw08d12.s1 NCJ CGAP_SST1 Homo sapiens cDNA clone IMAGE:1238519 3'
6982	19480	32301	2.2	2.0E-05	Y08926.1	NT	P. falciparum mRNA for AARP1 protein, partial
6994	19482	32313	1.34	2.0E-05	A1402960.1	EST_HUMAN	qc47h08.x1 NCJ CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711
7002	19500		8.08	2.0E-05	A891025.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN;
							hw35h07.x1 Soares_Diedgreffe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7207	19736	32591	2.2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7207	19738	32592	2.2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7403	19828		0.91	2.0E-05	AF128947.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
7828	20368	33276	1.41	2.0E-05	A361040.1	EST_HUMAN	h20h05.x1 NCJ CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2108389 3'
9191	21708	34651	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9191	21708	34652	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9837	22335	35317	0.48	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10041	22536	35532	0.74	2.0E-05	BF055639.1	EST_HUMAN	775g09.y1 NCJ CGAP_Bim20 Homo sapiens cDNA clone IMAGE:3340576 5'

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10482	22878	35884	2.62	2.0E-05	N41751.1	EST_HUMAN	yw61a06.r1 Soares_placenta_8to9weeks_2NkHP8a09W Homo sapiens cDNA clone IMAGE:256570 5'
10482	22878	35885	2.62	2.0E-05	N41751.1	EST_HUMAN	yw61a06.r1 Soares_placenta_8to9weeks_2NkHP8a09W Homo sapiens cDNA clone IMAGE:256570 5'
10524	19500		2.44	2.0E-05	A1891025.1	EST_HUMAN	w035r07.x1 Soares_Dieckgreife_cdon_NKCD Homo sapiens cDNA clone IMAGE:2522077 3'
11327	23025	36034	2.74	2.0E-05	BE175801.1	EST_HUMAN	RCS-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
11883	24844		4.81	2.0E-05	BE346228.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2;
12080	25018		13.02	2.0E-05	AW074804.1	EST_HUMAN	xs89a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element;
12144	24831		2.54	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12655	24727		2.35	2.0E-05	A1200970.1	EST_HUMAN	qf69j11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2719	15475	27841	1.45	1.0E-05	AL168282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3711	16312	28780	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Larinto 120 Suppressor of Hairless (Su(H)) gene, partial cds
4039	16637	29105	11.9	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4252	16840	29289	0.88	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4364	16951	28391	1.89	1.0E-05	AA431119.1	EST_HUMAN	zw68g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781464 5'
4876	17550	29882	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy48g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2656548 3'
5395	17853		0.94	1.0E-05	A1733588.1	EST_HUMAN	cs64d07.x5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1610125 3' similar to contains Alu repetitive element;
5428	17883	30389	0.91	1.0E-05	L27595.1	NT	Mus musculus bradykinin B2 receptor (B2R) gene, complete cds
6848	19438	32252	1.32	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7140	19520	32342	3.96	1.0E-05	AA841846.1	EST_HUMAN	ns19g02.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element;
7142	19675	32515	14.32	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7655	20167	33054	0.76	1.0E-05	BF222846.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_P-28 Homo sapiens cDNA clone IMAGE:3649045 3' similar to contains MER10.b3 MER10 repetitive element;
7754	20282		2.22	1.0E-05	P19474	SWISSPROT	S2 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8846	21385		2.56	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8890	21528	34457	2.18	1.0E-05	AA452578.1	EST_HUMAN	z36h12.x1 Soares_tet_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9211	21728	34671	13.74	1.0E-05	AA236110.1	EST_HUMAN	zs05a11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:384332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element;
9288	21888	34834	0.6	1.0E-05	AV732190.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTEB1H01 5'

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9752	22250	35232	0.76	1.0E-05	AW510902.1	EST_HUMAN	h411b02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element:
9752	22250	35233	0.76	1.0E-05	AW510902.1	EST_HUMAN	h411b02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element:
9830	22328	35309	1.58	1.0E-05	AW291521.1	EST_HUMAN	UH-B12-egk-a-08-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724388 3'
9830	22328	35310	1.58	1.0E-05	AW291521.1	EST_HUMAN	UH-B12-egk-a-08-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724388 3'
10087	22582		1.73	1.0E-05	AW468995.1	EST_HUMAN	h407c10.x1 NCI CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1 L2 L1 repetitive element:
10798	23322	36332	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
10798	23322	36333	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
12483	25011	30616	1.67	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
2698	15253	27824	4.74	9.0E-06	AI583811.1	EST_HUMAN	h73a06.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3130	15744	28213	5.23	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2N1HP8tc8W Homo sapiens cDNA clone IMAGE:1759191 3'
3670	16271		3.37	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6064	18881	31423	2.25	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6947	19524	32346	0.84	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-e07 BT0313 Homo sapiens cDNA
7466	19888	32853	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7751	20259	33156	12.47	9.0E-06	AI094370.1	EST_HUMAN	cc2dg01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element:
8400	20840	33863	1.18	9.0E-06	AL163309.2	NT	Homo sapiens chromosome 21 segment HS21C009
8913	21451	34372	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8913	21451	34373	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9149	21884	34828	4.8	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10616	23339	36353	3.76	9.0E-06	Q10384	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE GZE12.14C
2569	15469	27701	1.48	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-r11 CT0283 Homo sapiens cDNA
10424	22918	35919	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10424	22918	35920	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1015	13825		1.71	7.0E-08	AA689728.1	EST_HUMAN	ab60710.11 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1487	14080	26819	3.38	7.0E-08	7882177	NT	MER20.11 MER20 repetitive element ;
2177	14754	27324	1.55	7.0E-08	AW593215.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2897	15514		7.94	7.0E-08	A1388252.1	EST_HUMAN	hg11b12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2845279 3' similar to
3620	16223		1	7.0E-08	AA395542.1	EST_HUMAN	gb:XB2048_cds1 WEE1-LIKE PROTEIN KINASE (HUMAN);
5874	18486		5.81	7.0E-08	AW883141.1	EST_HUMAN	qw16g08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1891288 3' similar to contains Alu repetitive
5972	18593	31327	0.94	7.0E-08	N98845.1	EST_HUMAN	element;
8724	21283	34183	0.72	7.0E-08	11420708	NT	EST189205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
9814	22312		2.32	7.0E-08	Q61147	SWISSPROT	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
11710	25043	30508	1.62	7.0E-08	BF215972.1	EST_HUMAN	y65c07.1 Soares_multiple_sclerosis_2NBHMSHP Homo sapiens cDNA clone IMAGE:278412 5'
2942	15558	28032	1.29	8.0E-08	BE089189.1	EST_HUMAN	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF08S1E), mRNA
4885	15594	28085	2.03	8.0E-08	Q01456	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
4875	17450	28901	1.47	8.0E-08	A1040098.1	EST_HUMAN	601881622F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
5552	18184	30599	1.3	8.0E-08	AF167441.1	NT	QV3-BT0378-010300-105-411 BT0378 Homo sapiens cDNA
5805	18234	30885	1.15	8.0E-08	Q02040	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
9770	22288		1.67	8.0E-08	AW801912.1	EST_HUMAN	aa08a02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to
12802	24888	30881	1.47	8.0E-08	11418157	NT	contains MER8.12 MER8 repetitive element ;
5361	17921	30335	1.02	5.0E-08	AL163288.2	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
6211	18821	31592	3.73	5.0E-08	AL163246.2	NT	PROTEIN XE7
6479	19080	31883	2.04	5.0E-08	U07581.1	NT	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
7284	18812	32888	1.11	5.0E-08	AB007546.1	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
10013	22508	35499	6.57	5.0E-08	AA313820.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
10408	22800	35895	0.54	5.0E-08	P06881	SWISSPROT	Homo sapiens chromosome 21 segment HS21C048
12482	24615	30890	13.8	5.0E-08	A1065045.1	EST_HUMAN	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
675	13288	25780	6.05	4.0E-08	R18287.1	EST_HUMAN	Homo sapiens gene for LECT2, complete cds
879	13483	26011	6.94	4.0E-08	AW103354.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
							COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
							HA0877 Human fetal liver cDNA library Homo sapiens cDNA
							ye48c03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu
							repetitive element; contains L1 repetitive element ;
							xx68g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu
							repetitive element; contains element MER21 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1379	13872	28469	3.92	4.0E-06	AF334928.1	EST_HUMAN	h33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1379	13872	28500	3.92	4.0E-06	AF334928.1	EST_HUMAN	h33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1522	14114	28851	3.17	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200800-250-107 NT0046 Homo sapiens cDNA
2305	14878	27454	1.68	4.0E-06	AW015401.1	EST_HUMAN	U1-H-BIO-east-4-05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3099	15714	28186	1.26	4.0E-06	AF188349.1	NT	Gallus gallus Dact12 protein (Dact12) mRNA, complete cds
3963	16561	28030	1.35	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-803 CT0214 Homo sapiens cDNA
4930	17505	28851	1.88	4.0E-06	AB86839.1	EST_HUMAN	w84c10.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
5053	17628	30070	2.12	4.0E-06	AL163279.2	NT	MER22 repetitive element;
8438	20878	33890	0.53	4.0E-06	Q15393	SWISSPROT	Homo sapiens chromosome 21 segment HS21C079
8735	21274	34195	2.68	4.0E-06	AF088680.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
8824	22124	35088	1.11	4.0E-06	AJ272265.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11324	23022	36031	3.84	4.0E-06	AB007055.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2208	14784	27357	1.31	3.0E-06	AA700562.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2208	14784	27358	1.31	3.0E-06	AA700562.1	EST_HUMAN	z54b08.s1 Scores_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.11 L1 repetitive element;
2307	14879		1.54	3.0E-06	AF202635.1	NT	z54b08.s1 Scores_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.11 L1 repetitive element;
2948	15584	28038	1.02	3.0E-06	AA868218.1	EST_HUMAN	Homo sapiens PP1200 mRNA, complete cds
3304	15915		2.41	3.0E-06	AB57779.1	EST_HUMAN	ak48g11.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13
3651	16449	28911	1.08	3.0E-06	BE047094.1	EST_HUMAN	LTR1 repetitive element;
3651	16449	28912	1.08	3.0E-06	BE047094.1	EST_HUMAN	wf22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734
4573	17156	28600	0.68	3.0E-06	T50286.1	EST_HUMAN	LINE-1 LIKE PROTEIN :contains L1.12 L1 repetitive element;
4661	17243	28697	4.82	3.0E-06	X54816.1	NT	LINE-1 LIKE PROTEIN :contains L1.12 L1 repetitive element;
5045	17618	30063	0.94	3.0E-06	J04038.1	NT	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
5045	17618	30064	0.94	3.0E-06	J04038.1	NT	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6308	18915	31689	0.78	3.0E-06	AU159412.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
7280	18908		2.79	3.0E-06	P08548	SWISSPROT	y078b10.11 Strabagene ovary (#637217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
8027	20569	33473	0.72	3.0E-06	BE562864.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
8618	21157	34070	0.69	3.0E-06	P07743	SWISSPROT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
							Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
							Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
							AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001802 3'
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							801336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680314 5'
							PAROTID SECRETORY PROTEIN PRECURSOR (PSP)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12162	24394		13.37	3.0E-06	AW365262.1	EST_HUMAN	RCO-LT0001-261169-011-A03 LT0001 Homo sapiens cDNA
216	12877		2.91	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1614	14207		4.48	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2418	14980	27530	2.2	2.0E-06	A1672138.1	EST_HUMAN	w804603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element;
2506	15070	27643	1.79	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2601	15163	27731	1.34	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3570	16174	28656	1.04	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3825	16425	28887	1.85	2.0E-06	AA173518.1	EST_HUMAN	zp02605.t1 Stratiotes ovata cancer (#637219) Homo sapiens cDNA clone IMAGE:595232 5'
3838	16435	28897	0.63	2.0E-06	AW450215.1	EST_HUMAN	U-H-B13-alky-9-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3844	16443	28904	1.74	2.0E-06	AB030898.1	NT	Mus musculus gene for odorant receptor A18, complete cds
6239	18848		0.78	2.0E-06	AA974632.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6267	18875	31643	0.87	2.0E-06	A1539448.1	EST_HUMAN	ts51805.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080241 3' similar to TRQ13537
6570	19168	31965	4.94	2.0E-06	A1819424.1	EST_HUMAN	Q13537 MER37 TRANSDUCIBLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7858	20400		0.89	2.0E-06	AW869223.1	EST_HUMAN	w808004.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8033	20575	33480	0.75	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA
8770	21309		0.59	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447 zh27c11.s1 Soares_pined_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
8782	21321	34245	1.54	2.0E-06	H62051.1	EST_HUMAN	yu37c04.r1 Soares ovary NBHOT Homo sapiens cDNA clone IMAGE:235674 5' similar to gb:X74929
9143	21678	34621	0.91	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9143	21678	34622	0.91	2.0E-06	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9817	22117	35080	0.72	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9833	22331		0.63	2.0E-06	AV748969.1	EST_HUMAN	yu68a03.s1 Soares_placenta_8to8weeks_2NBHP609W Homo sapiens cDNA clone IMAGE:267212 3'
12052	25046	30508	1.61	2.0E-06	P23249	SWISSPROT	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
12210	24434		6.63	2.0E-06	BE328232.1	EST_HUMAN	PROTEIN MOV-10 hs0202.x1 NCI_CGAP_Ku13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1 repetitive element ;
36	12715	25174	1.77	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
685	13309	25794	1.45	1.0E-06	AF084384.1	NT	Mus musculus D6M45E protein (D6M45e) mRNA, complete cds
1500	14092	26631	2.08	1.0E-06	P08125	SWISSPROT	MEROZOITE SURFACE PROTEIN GMZ-8

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1571	14164	26895	1.12	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1627	14220		1.54	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2037	14619	27186	8.38	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2037	14619	27187	8.38	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4459	17045	29488	14.7	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5269	17831	30256	0.99	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5269	17831	30257	0.99	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5494	18128	30536	4.64	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5518	18150	30563	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5518	18150	30564	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5687	18294	30774	1.13	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6854	19631	32358	5.98	1.0E-06	P02871	SWISSPROT	FIBRINOGEN ALPHA2(II) CHAIN PRECURSOR
7943	20486		0.68	1.0E-06	AA012823.1	EST_HUMAN	d23-08.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8216	20757	33071	1.21	1.0E-06	AS47010.1	EST_HUMAN	qp54-02.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3'
8425	20985	33879	1.23	1.0E-06	AL287878.1	EST_HUMAN	q23108.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9228	21950	34889	0.88	1.0E-06	N74635.1	EST_HUMAN	MIR repetitive element;
9301	21901	34850	0.5	1.0E-06	Q39575	SWISSPROT	zs55-01.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286472 3'
9600	22100	35062	3.34	1.0E-06	U82668.1	NT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9600	22100	35063	3.34	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9843	22143	35111	4.36	1.0E-06	AA132611.1	EST_HUMAN	Homo sapiens shox gene, alternatively spliced products, complete cds
9703	22202		3.84	1.0E-06	AA448257.1	EST_HUMAN	zo17-08.r1 Stragene colon (8637204) Homo sapiens cDNA clone IMAGE:587174 5'
10382	22876		1.61	1.0E-06	AL163203.2	NT	zo04d11.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:587174 5'
11502	23951		8.24	1.0E-06	AW890941.1	EST_HUMAN	gb:D28128 RIBONUCLEASE PANGREATIC PRECURSOR (HUMAN);
12087	24356	30966	7.83	1.0E-06	L78810.1	NT	Homo sapiens chromosome 21 segment HS21C003
12185	14619	27186	1.67	1.0E-06	AF184614.1	NT	RC4-NT0054-120500-012-503 NT0054 Homo sapiens cDNA
12185	14619	27187	1.67	1.0E-06	AF184614.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12803	14220		1.38	1.0E-06	P27625	SWISSPROT	Homo sapiens p47-phox (NCF1) gene, complete cds
383	13030	25518	2.01	9.0E-07	AF003528.1	NT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
383	13030	25519	2.01	9.0E-07	AF003528.1	NT	Homo sapiens gypican 3 (GPC3) gene, partial cds and flanking repeat regions
8346	20887		0.57	9.0E-07	AL163280.2	NT	Homo sapiens gypican 3 (GPC3) gene, partial cds and flanking repeat regions
11126	23634	36075	2.65	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C081

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4885	17460	28912	5.02	8.0E-07	AI288588.1	EST_HUMAN	q82g07.x1 Soares_NH-MIPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
4885	17460	28913	5.02	8.0E-07	AI288588.1	EST_HUMAN	q82g07.x1 Soares_NH-MIPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'
6047	18688		7.48	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
7044	20486		9.51	8.0E-07	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11488	23835		8.73	8.0E-07	T07770.1	EST_HUMAN	EST056860 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBEN89
11680	24106		7.98	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1806	14481	27052	1.14	7.0E-07	AF167341.1	NT	Homo sapiens membrane Interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5710	18336	30841	0.89	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5710	18336	30842	0.89	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
10842	23174	36188	1.59	7.0E-07	BE676848.1	EST_HUMAN	733g01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3288468 3' similar to TR-Q96897 Q96897
1858	14540	27038	2.56	8.0E-07	AW855558.1	EST_HUMAN	ENDOGENOUS RETROVIRUS-K, LTR U5 AND GAG GENE. ;
							CN3-CT0277-221068-024-e11 CT0277 Homo sapiens cDNA
2534	15038	27671	2.3	6.0E-07	AF018413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytotochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
4044	18842		1.78	8.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9088	21605	34538	1.94	6.0E-07	BF001887.1	EST_HUMAN	7g84f07.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR-O75820 O75820
11625	24087	37131	1.83	6.0E-07	AI782850.1	EST_HUMAN	4F5L. ;
11949	24989		2.85	6.0E-07	AW803222.1	EST_HUMAN	om87f05.y6 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1554177 5'
348	12888		1.19	5.0E-07	AU831883.1	EST_HUMAN	OM4-NN1029-260300-121-h12 NN1029 Homo sapiens cDNA
1095	13700		2.21	5.0E-07	AA380630.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
3068	15881		0.94	5.0E-07	AU831883.1	EST_HUMAN	EST03815 Supt cells Homo sapiens cDNA 5' end
4751	17332	29775	1.32	5.0E-07	AF149774.1	NT	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
6288	18878	31644	1.13	5.0E-07	U85067.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
7124	19484	32281	1.56	5.0E-07	AI393981.1	EST_HUMAN	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7124	19484	32282	1.56	5.0E-07	AI393981.1	EST_HUMAN	ig08f05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu
7388	18812	32776	16.07	5.0E-07	AW070885.1	EST_HUMAN	repetitive element/contains element A3R repetitive element ;
8217	20758	33672	0.82	5.0E-07	O9WUQ1	SWISSPROT	ig08f05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu
							repetitive element/contains element A3R repetitive element ;
							ig08f05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2588342 3' similar to gb.X15341
							CYTOTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
							ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
							MOTIFS 1) (ADAMTS-1) (ADAM-TS1)

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8427	20967		1.06	5.0E-07	P09583	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10270	22765	35752	4.46	5.0E-07	A1808597.1	EST_HUMAN	CM-BT178-220469-014 BT178 Homo sapiens cDNA
10542	23079	36093	1.56	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11391	23843	36907	4.04	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11452	23902		2.43	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12391	24889		2.85	5.0E-07	AW882537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4071	16867	28129	1.94	4.0E-07	AW009602.1	EST_HUMAN	w84h05.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2504697 3'
7230	19761		0.98	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7311	19839	32697	1.35	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7311	19839	32698	1.35	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7863	20405	33312	0.65	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8681	21519	34445	5.37	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu04.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10228	22723	35715	0.5	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10617	23338	36351	4.05	4.0E-07	AJ765528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3'
10817	23338	36352	4.05	4.0E-07	AJ765528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3'
11100	23610		2.08	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
							Human microfilament-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced untranslated exons
488	13100	25591	4.51	3.0E-07	U19718.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
609	13237	25711	2.84	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1417	14010	28539	1.65	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
1667	14260		1.95	3.0E-07	M84857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
							n55b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element;
2090	14670		3.87	3.0E-07	AA526763.1	EST_HUMAN	Human polymorphic microsatellite DNA
2327	14898	27471	1.72	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
2508	15072	27845	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2508	15072	27846	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3099	15684	28156	0.79	3.0E-07	T84704.1	EST_HUMAN	y450f12.l1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111695 5'
3195	15907	28280	2.03	3.0E-07	P38739	SWISSPROT	HYPOTHEICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4788	17368		0.58	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)
4834	17412	28865	7.74	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLC00001 3'
4878	17453	28865	0.71	3.0E-07	AJ797236.1	EST_HUMAN	w86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
							yc14f09.s1 Strathene lung (8837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M82982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5222	17787	30205	1.81	3.0E-07	T57650.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5222	17787	30208	1.81	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:1462982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5847	18471	31197	12.78	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6128	18743	31488	0.71	3.0E-07	O42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6804	18395		5.41	3.0E-07	AA815175.1	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7519	20039	32808	3.22	3.0E-07	AW787168.1	EST_HUMAN	cc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1330890 3'
7659	20171		1.8	3.0E-07	AI591065.1	EST_HUMAN	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
11373	23825		1.88	3.0E-07	BE439409.1	EST_HUMAN	hw28f11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
12841	24716		6.74	3.0E-07	AJ132352.1	NT	HTMH-025F1 HTM1 Homo sapiens cDNA
31	12710	25168	3.36	2.0E-07	AF282888.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
165	12828	25314	7.91	2.0E-07	L77588.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
165	12828	25315	7.91	2.0E-07	L77588.1	NT	Homo sapiens DRGeorge syndrome critical region, telomeric end
194	12854	25338	45.53	2.0E-07	U38949.1	NT	Homo sapiens DRGeorge syndrome critical region, telomeric end
778	13397	25898	2.58	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
778	13397	25898	2.58	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
791	13409		0.81	2.0E-07	P11369	SWISSPROT	ENDONUCLEASE]
979	13591	28108	2.56	2.0E-07	AA223280.1	EST_HUMAN	z08b07.s1 Stragene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:650888 3' similar to gb:131880 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
980	13592	28107	6.66	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element ;
1205	13805	28318	0.76	2.0E-07	Q26788	SWISSPROT	I68 AUTOANTIGEN
1644	14236	26771	1.88	2.0E-07	Q08701	SWISSPROT	HYPOTHELICAL 72.6 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3679	16280		0.65	2.0E-07	BF131397.1	EST_HUMAN	801818818F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3751	16352	28820	22.38	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5547	18178	30583	1.81	2.0E-07	AW88068.1	EST_HUMAN	RC3-NIN0068-260400-021-g11 NIN0068 Homo sapiens cDNA
6769	19382	32171	1.59	2.0E-07	AI208715.1	EST_HUMAN	qq56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8405	20946		3.67	2.0E-07	AV728390.1	EST_HUMAN	AV728390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8528	21167	34082	1.1	2.0E-07	AA035188.1	EST_HUMAN	z627g08.s1 Soares_pregnant_uterus_Nht-IPU Homo sapiens cDNA clone IMAGE:471808 3'
8878	22175		2.27	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10168	22863	35658	5.85	2.0E-07	AW892507.1	EST_HUMAN	GM4-NIN003-280300-124-e08 NIN003 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10383	22877	35888	0.76	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
10383	22877	35888	0.75	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11842	24603		2.57	2.0E-07	BE153717.1	EST_HUMAN	PMO-HT03339-260100-008-H07 HT0339 Homo sapiens cDNA
11734	24890		3.56	2.0E-07	A1732462.1	EST_HUMAN	zr58h11.x6 Strabegene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565028 3' similar to contains THR.b2 THR repetitive element:
1141	13744		1.17	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2013	14595	27157	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2013	14595	27158	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2424	14892	27565	0.93	1.0E-07	P10283	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2854	14162	28883	2.94	1.0E-07	P08266	SWISSPROT	GLYCOPROTEIN GPV
3807	13744		1.22	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4380	16987	29413	2.75	1.0E-07	AV178882.1	EST_HUMAN	AV178882 GLC Homo sapiens cDNA clone GLCFNF04.6
4380	16987	29414	2.75	1.0E-07	AV178882.1	EST_HUMAN	AV178882 GLC Homo sapiens cDNA clone GLCFNF04.5
6827	19223	32028	1.57	1.0E-07	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6850	19527	32349	4.57	1.0E-07	BE047871.1	EST_HUMAN	bx43d06.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291339 5'
6850	19527	32350	4.57	1.0E-07	BE047871.1	EST_HUMAN	bx43d06.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291339 5'
7504	20028	32890	8.62	1.0E-07	N55081.1	EST_HUMAN	y43607.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7644	20156	33042	0.82	1.0E-07	BF375809.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
7644	20156	33043	0.82	1.0E-07	BF375809.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
7669	20181	33068	1.35	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8157	20688	33611	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8157	20688	33612	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8884	21422	34347	2.7	1.0E-07	AA683578.1	EST_HUMAN	z51e10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:434348 3'
9104	21711	34654	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9535	22035	34995	0.49	1.0E-07	BE327843.1	EST_HUMAN	huz28r08.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9849	22347	35329	2.51	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element:
9855	22353	35334	1.19	1.0E-07	AA396311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
10362	22856		3.53	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C082

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12013	24860	30704	2.42	1.0E-07	BE048770.1	EST_HUMAN	h53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:065722 065722
7325	19852	32714	0.87	9.0E-08	AI539362.1	EST_HUMAN	DJ116311.1;
6802	22300	35285	2.1	9.0E-08	AV734818.1	EST_HUMAN	le51b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
11091	23573	36610	3.41	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cdA Homo sapiens cDNA clone cDABF808 5'
11519	23967	37039	4.51	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
11981	24283		2.98	9.0E-08	AJ251973.1	NT	OFR repetitive element;
635	15420		2.27	8.0E-08	AI811352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1068	13693		0.79	8.0E-08	BE795468.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
3568	16202		1.05	8.0E-08	BE795468.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8674	21213	34133	3.54	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
8674	21213	34134	3.54	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
8545	22045	35008	3.32	8.0E-08	AW1970683.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11124	23632		2.81	8.0E-08	AF253417.1	NT	EST382778 MAGE resequences, MAGK Homo sapiens cDNA
84	12780	25243	2.82	7.0E-08	Q02357	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1405	13968	26527	11.08	7.0E-08	X04808.1	NT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
3635	16238	28713	0.7	7.0E-08	P15305	SWISSPROT	Rat mRNA for ribosomal protein L31
3635	16238	28714	0.7	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
4002	16600	28073	0.89	7.0E-08	P01808	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
4002	16600	28074	0.89	7.0E-08	P01806	SWISSPROT	IG KAPPA CHAIN V4 REGION OU
10693	23223		6.5	7.0E-08	AI535743.1	EST_HUMAN	IG KAPPA CHAIN V4 REGION OU
11523	23971	37041	6.1	7.0E-08	U24070.1	NT	cong3.P11.A5 conom Homo sapiens cDNA 3'
12450	16238	28713	3.59	7.0E-08	P15305	SWISSPROT	Rattus norvegicus Munc13-1 mRNA, complete cds
12450	16238	28714	3.59	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
850	13466	25974	3.81	6.0E-08	AL163248.2	NT	DYNEIN HEAVY CHAIN (DYHC)
850	13466	25975	3.81	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2401	14969	27543	2.01	6.0E-08	BE144398.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
4334	16921	28363	1.14	6.0E-08	AL163248.2	NT	MRO-HT0168-191189-004-g09 HT0168 Homo sapiens cDNA
7892	20434		0.68	6.0E-08	P08547	SWISSPROT	Homo sapiens chromosome 21 segment HS21C048
9251	21777		0.6	6.0E-08	AA827075.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							cb56605.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1335388 3' similar to contains
							MER12.b3 MER12 repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11233	23745	36802	2.61	6.0E-08	P11368	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11407	23858		1.77	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
88	12784	25247	2.33	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2277	14851	27429	1.23	5.0E-08	AA469351.1	EST_HUMAN	nt003b09.at1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element;
11692	24107		7.32	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
11688	24233	31004	1.48	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131088-034-a12 CT0225 Homo sapiens cDNA
1787	14387	26831	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1787	14387	26832	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2810	15527		1.49	4.0E-08	AL079681.1	EST_HUMAN	DKFZp434J0428_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J0428 5'
3100	15715		1.01	4.0E-08	AI078417.1	EST_HUMAN	cd05402.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
3886	16584	29055	0.67	4.0E-08	UB26988.1	NT	Homo sapiens short gene, alternatively spliced products, complete cds
6537	19136	31929	1.14	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8733	21272	34182	0.57	4.0E-08	O15383	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9068	21803	34533	0.92	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9563	22063		0.87	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10233	22728		0.71	4.0E-08	AI016342.1	EST_HUMAN	cd78d12.at1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1622903 3'
10287	22782	35774	3.59	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
10782	23306		1.7	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
10968	23483	36510	3.7	4.0E-08	BF682493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
10968	23483	36511	3.7	4.0E-08	BF682493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11697	25022		1.4	4.0E-08	W76159.1	EST_HUMAN	z885g03.r1 Soares_fetal_liver_NbH119W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element;
12378	24546		3.48	4.0E-08	AJ343353.1	EST_HUMAN	tb85a11.x1 NCI_CGAP_Cor16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element;
5785	18420	31136	3.12	3.0E-08	BE018348.1	EST_HUMAN	b578a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TRC9Z158 Q8Z158
7052	18071	30462	3.77	3.0E-08	AJ792737.1	EST_HUMAN	qs78f11.y6 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1944045 5'
7545	20065	32939	1.41	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7730	20238		4.17	3.0E-08	AK36352.1	EST_HUMAN	th83h08.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8812	22310		0.51	3.0E-08	AF055086.1	NT	Homo sapiens MHC class 1 region
11882	24087		38.85	3.0E-08	R18420.1	EST_HUMAN	y02804.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
220	12881		6.74	2.0E-08	AW302886.1	EST_HUMAN	jr8706.x1 NCL CGAP_L1281 Homo sapiens cDNA clone IMAGE:2767139 3'
247	12907		6.48	2.0E-08	AA425588.1	EST_HUMAN	zw4807.r1 Scores total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element/contains element MER15 repetitive element ;
522	13164	25637	2.59	2.0E-08	AF188348.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
688	13312	25786	10.98	2.0E-08	AW888438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
688	13312	25797	10.98	2.0E-08	AW888438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1027	13638		22.68	2.0E-08	BE280477.1	EST_HUMAN	60115321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138868 5'
1387	13981	26508	2.09	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1777	14387		1.3	2.0E-08	BE734871.1	EST_HUMAN	801670463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845189 5'
1895	14480		4.65	2.0E-08	AW270271.1	EST_HUMAN	xp45f11.x1 NCL CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2462	15028	27587	0.97	2.0E-08	AA731948.1	EST_HUMAN	mw64h01.s1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:1281408 3' similar to contains L1.L3 L1 repetitive element ;
2580	15143		2.21	2.0E-08	K00218.1	NT	Sheep His-RNA-GUG
3243	15855	28337	6.85	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3243	15855	28338	6.85	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3928	16524		1.93	2.0E-08	AW813820.1	EST_HUMAN	RC3-ST0187-161089-012-503 ST0187 Homo sapiens cDNA
4152	16744	28188	0.57	2.0E-08	U82888.1	NT	Homo sapiens afbx gene, alternatively spliced products, complete cds
4494	17079		1.74	2.0E-08	AA458040.1	EST_HUMAN	sa28c07.r1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.L2 L1 repetitive element ;
5082	17885		3.83	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5817	18441	31163	0.87	2.0E-08	AA813204.1	EST_HUMAN	ai80h11.s1 Scores testis_NHT Homo sapiens cDNA clone 1377189 3'
5898	18618	31354	0.87	2.0E-08	AW088924.1	EST_HUMAN	xx32c04.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595482 3' similar to contains MER18.b3
7945	20488	33388	1.07	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element ;
8054	20598	33503	1.2	2.0E-08	AA490121.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE, ENDONUCLEASE]
8014	21551		1.41	2.0E-08	AU139978.1	EST_HUMAN	ak02p08.a1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839874 3'
							AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	22807	35804	0.78	2.0E-08	N78087.1	EST_HUMAN	y7202.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contig...
10413	22807	35805	0.78	2.0E-08	N78087.1	EST_HUMAN	LTR1.63 LTR1 repetitive element;
11882	24283		1.74	2.0E-08	AL163284.2	NT	y7202.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains
							LTR1.63 LTR1 repetitive element;
							Homo sapiens chromosome 21 segment HS21C084
12559	25073		1.44	2.0E-08	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide
1812	14402	26947	0.98	1.0E-08	AF125348.1	EST_HUMAN	4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
2095	14674		2.74	1.0E-08	BE141658.1	EST_HUMAN	polypeptide 5 (CYP3A5) gene, partial cds
5785	18410	31128	4.23	1.0E-08	AJ010770.1	NT	Homo sapiens carotid 1 (CAV1) gene, exon 3 and partial cds
7748	20254	33148	1.14	1.0E-08	P19474	SWISSPROT	PM2-HT0130-150888-001-112 HT0130 Homo sapiens cDNA
7978	20520	33428	0.55	1.0E-08	AL163302.2	NT	Homo sapiens hyperion gene, exons 1-50
							82 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8070	20612	33525	0.85	1.0E-08	AF224688.1	NT	Homo sapiens chromosome 21 segment HS21C102
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8070	20612	33526	0.85	1.0E-08	AF224688.1	NT	(UBE2D3) genes, complete cds
8484	21023	33940	1.84	1.0E-08	AJ015304.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
9132	21687	34608	0.75	1.0E-08	BE072572.1	EST_HUMAN	(UBE2D3) genes, complete cds
							Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
9878	22373	35350	1.16	1.0E-08	P78110	SWISSPROT	(UBE2D3) genes, complete cds
10449	22843	35833	0.84	1.0E-08	P98083	SWISSPROT	cd35a05.s1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1618738 3'
11105	23700	36751	3.79	1.0E-08	AF044083.1	NT	PM2-BT0546-210100-004-002 BT0546 Homo sapiens cDNA
12081	24353		2.27	1.0E-08	X51755.1	NT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
4327	16813	28356	3.93	9.0E-08	AL163278.2	NT	(TRICARBOXYLATE CARRIER PROTEIN)
4327	16813	28357	3.93	9.0E-08	AL163279.2	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
8974	22469		0.49	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
							Homo sapiens lambda-immunoglobulin constant region complex (germline)
7308	19838	32894	8.83	8.0E-08	AI183500.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7942	20484	33396	2.88	8.0E-09	AW600159.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
8919	21457		2.77	8.0E-08	AA838882.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121818 3'
							ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121818 3'
							ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121818 3'
3687	16288		1.87	7.0E-08	D68842.1	NT	contains MSR1.11 MSR1 repetitive element;
4080	16678		1	7.0E-09	U50871.1	NT	CA0-NN1004-100300-273-c08 NN1004 Homo sapiens cDNA
							op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
							Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
							[Human familial Alzheimer's disease (STM2) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7843	20385		0.5	7.0E-08	BF108755.1	EST_HUMAN	745e10.x1 Soares NSF_F8_GW_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
7991	20533		0.78	7.0E-08	AA256200.1	EST_HUMAN	zf60c05.r1 Soares NIHMFU_S1 Homo sapiens cDNA clone IMAGE:681882 5' similar to contains L1.12 L1 repetitive element;
8184	21701	34844	2.88	7.0E-08	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10088	22581	35574	1.3	7.0E-08	BE264850.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10248	22743		0.83	7.0E-08	AA058826.1	EST_HUMAN	zf58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381158 3' similar to contains L1.12 L1 repetitive element;
10552	23088		2.78	7.0E-08	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121818 3'
2188	14774		1.16	6.0E-08	AL040438.1	EST_HUMAN	DKFZp434C0514.1 434 (synonym: hbas3) Homo sapiens cDNA clone DKFZp434C0514 5'
5118	17688	30128	5.44	6.0E-08	BE188421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
5246	17810	30232	1	6.0E-08	AW593471.1	EST_HUMAN	hg18f12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:53743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5248	17810	30233	1	6.0E-08	AW593471.1	EST_HUMAN	hg18f12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:53743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5582	18213	30662	12.11	6.0E-08	AW185784.1	EST_HUMAN	xn85h08.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8512	21051	33973	0.81	6.0E-08	BE161653.1	EST_HUMAN	MR3-HT0448-280300-201-h12 HT0448 Homo sapiens cDNA
9103	21838	34578	2.37	6.0E-08		NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10177	22872		3.89	6.0E-08	AF200823.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10910	23143	36154	1.88	6.0E-08	BF108755.1	EST_HUMAN	745e10.x1 Soares NSF_F8_GW_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
1480	14052	26584	3.95	5.0E-08	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1883	14478	27038	0.93	5.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6542	18141	31833	2.28	5.0E-08	AA359454.1	EST_HUMAN	EST168746 Fetal lung II Homo sapiens cDNA 5' end
8521	21060	33983	0.59	5.0E-08	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10007	22502	35483	2.27	5.0E-08	AW786687.1	EST_HUMAN	PM2-UM0053-240300-006-c09 UM0053 Homo sapiens cDNA
547	13178		1.89	4.0E-08	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1000	13611		1.89	4.0E-08	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
1518	14110	28648	1.81	4.0E-08	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2473	15040	27608	4.54	4.0E-08	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
7788	20331	33237	0.72	4.0E-08	AA495747.1	EST_HUMAN	zn04c08.r1 Soares NIHMFU_S1 Homo sapiens cDNA clone IMAGE:788298 5'
8458	20688	33915	0.62	4.0E-08	TC4942.1	EST_HUMAN	yd11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:68804 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10896	23510		1.73	4.0E-09	AA195142.1	EST_HUMAN	x344r12.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:985278 5' similar to gb:L07807
2390	14958	27530	6.83	3.0E-09	BE222239.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
2589	15151	27717	0.86	3.0E-09	BE222239.1	EST_HUMAN	h09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2677	15235	27802	1.22	3.0E-09	P23249	EST_HUMAN	MER18 repetitive element;
3372	15980	28457	1.05	3.0E-09	BE222239.1	EST_HUMAN	h09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3423	16031		3.13	3.0E-09	AA44272.1	EST_HUMAN	PROTEIN MOV-10
4172	16763		3.54	3.0E-09	X16874.1	NT	h09609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
4517	17101	29548	5.18	3.0E-09	AF175325.1	NT	MER18 repetitive element;
4610	17193	29639	1.52	3.0E-09	Q873R5	SWISSPROT	z65404.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
7841	20363	33287	1.28	3.0E-09	BE465780.1	EST_HUMAN	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
10146	22641	35631	1.98	3.0E-09	AL163247.2	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
10900	23420	36437	3.87	3.0E-09	BF108943.1	EST_HUMAN	258.1 KDA PROTEIN C21ORF5 (KIAA0893)
10900	23420	36438	3.87	3.0E-09	BF108943.1	EST_HUMAN	h080402.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3184090 3' similar to TR:O55091
845	13461		1.01	2.0E-09	X16874.1	NT	O55091 IMPACT PROTEIN.;
1301	13885	28417	6.02	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1698	14291		10.31	2.0E-09	AL118573.1	EST_HUMAN	DKFZp781B1710_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781B1710 5'
2364	14835	27507	2.79	2.0E-09	Q873R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0893)
4011	16909	29082	4.13	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4083	16378	28139	0.94	2.0E-09	AI283478.1	EST_HUMAN	q07609.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
6676	19610		0.74	2.0E-09	AA357407.1	EST_HUMAN	EST68142 Kidney IX Homo sapiens cDNA 5' and similar to EST containing L1 repeat
7474	19986	32861	8.48	2.0E-09	AA481430.1	EST_HUMAN	z63306.r1 Soares_tadus_Nb23-IF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains
7532	20052	32925	0.68	2.0E-09	W28634.1	EST_HUMAN	Alu repetitive element;
8646	21185	34104	1.72	2.0E-09	AJ271735.1	NT	52411 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11634	24074		1.72	2.0E-09	AF111168.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12238	13461		27.08	2.0E-09	X16874.1	NT	Homo sapiens sarine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
12310	25084		2.25	2.0E-09	AA226070.1	EST_HUMAN	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
							nc11602.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1032	13642		1.14	1.0E-09	W78152.1	EST_HUMAN	z078003.s1 Soares_fetal_heart_NIH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to
1148	13751	26280	2.3	1.0E-09	5031824	NT	gb102932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1148	13751	26281	2.3	1.0E-09	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2914	15531	28003	1.74	1.0E-09	U80017.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2952	15568	28042	3.98	1.0E-09	M28699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory
2952	15568	28043	3.98	1.0E-09	M28699.1	NT	protein (hnp) and survival motor neuron protein (smn) genes, complete cds
3073	15688	28160	0.77	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
							Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
4816	17491		5.48	1.0E-09	AA719287.1	EST_HUMAN	601058802F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
5694	18320	30819	0.87	1.0E-09	AL163283.2	NT	z035903.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains
5698	18816	31352	1.48	1.0E-09	U07000.1	NT	Alu repetitive element; contains element MER22 repetitive element;
6283	18901	31871	3.17	1.0E-09	P28694	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
8328	20870	33794	0.87	1.0E-09	AJ689474.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
10216	22711		2.57	1.0E-09	AL163283.2	NT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
12136	25032	30820	3.3	1.0E-09	11418127	NT	w038005.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
12593	24944		1.82	1.0E-09	AF260225.1	NT	MER25.11 MER25 repetitive element;
1352	13947	26471	1.48	9.0E-10	AW867740.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
							Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2860	15479	27955	6.87	9.0E-10	AU870071.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6922	19581	32410	4.35	9.0E-10	AJ452982.1	EST_HUMAN	MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
158	12821	25309	10.47	8.0E-10	U63630.2	NT	w078h03.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
3368	15965	28472	0.69	8.0E-10	BE080748.1	EST_HUMAN	SW_RL28_HUMAN P47914 60S RIBOSOMAL PROTEIN L28; contains element PTR5 repetitive element;
4279	18865	28311	4.11	8.0E-10	AA376832.1	EST_HUMAN	Y48b09.x1 Soares_NSF_FB_PW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
9875	22372		2.34	8.0E-10	U36308.2	NT	TR-C00372 C00372 PUTATIVE P150;
730	13350	25844	24.94	7.0E-10	7706225	NT	Homo sapiens MCMA4 (MCMA) and DNA-PKcs (PRKDC) genes, partial cds
730	13350	25845	24.94	7.0E-10	7706225	NT	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
1893	14256	26791	2.13	7.0E-10	Q13342	SWISSPROT	EST86564 Small intestine [Homo sapiens cDNA 5' end
2067	14847		1.31	7.0E-10	P08548	SWISSPROT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
2594	15156		13	7.0E-10	P08547	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
							Homo sapiens TPA inducible protein (LOC51586), mRNA
							LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3124	15738	28206	2.84	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
6332	18938	31714	5.26	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
7446	18970	32838	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-208-D12 HT0619 Homo sapiens cDNA
7652	20184		1.43	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7916	20458	33364	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
7916	20458	33365	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10212	22707	35701	0.57	7.0E-10	L08885.1	NT	Homo sapiens MAD5MEF2-family transcription factor (MEF2C) mRNA, complete cds
11511	23858	37030	1.54	7.0E-10	AW778789.1	EST_HUMAN	h012602.x1 NCI_CGAP_C014 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Alu repetitive element; contains MER7.b1 MER7 repetitive element ;
948	13558	28072	3.68	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2702	15258	27827	1.89	6.0E-10	AJ424405.1	EST_HUMAN	h02007.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2085021 3'
4847	17425		2.15	6.0E-10	AW653718.1	EST_HUMAN	RC3-C10254-031088-012-g12 C10254 Homo sapiens cDNA
8718	21257	34177	0.94	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8718	21257	34178	0.94	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E)
9552	22052	35015	0.52	6.0E-10	P38073	SWISSPROT	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
11731	24136		1.47	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE reassessances, MAGL Homo sapiens cDNA
782	13410		5.2	6.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5'
3522	16127	28607	0.96	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
5002	17575	30018	1.05	5.0E-10	AW028877.1	EST_HUMAN	h097603.x1 NCI_CGAP_G084 Homo sapiens cDNA clone IMAGE:2542061 3' similar to contains MER10.11 repetitive element ;
5002	17575	30019	1.05	5.0E-10	AW028877.1	EST_HUMAN	h097603.x1 NCI_CGAP_G084 Homo sapiens cDNA clone IMAGE:2542061 3' similar to contains MER10.11 repetitive element ;
5128	17700	30134	1.37	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7363	18888		1.84	5.0E-10	BF105159.1	EST_HUMAN	60182218AF1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9455	21881	34832	1.65	5.0E-10	P34878	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
9455	21881	34833	1.65	5.0E-10	P34878	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
116	12787		1.02	4.0E-10	A1221083.1	EST_HUMAN	g008009.x1 Soares_pleocenta_85cweeks_2N1bHP81c9W Homo sapiens cDNA clone IMAGE:1758049 3' similar to contains LTR8.b2 LTR8 repetitive element ;
607	13235	25708	0.73	4.0E-10	AA515280.1	EST_HUMAN	h044601.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:924648 3'
2039	14821	27189	1.17	4.0E-10	AW584709.1	EST_HUMAN	h058603.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2946844 3' similar to contains Alu repetitive element

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15171	27739	4.19	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
7228	19759	32614	22.35	4.0E-10	AF224998.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10097	22582	35584	0.82	4.0E-10	AW263243.1	EST_HUMAN	U1H-B12-af-a-07-Q-U1.s1 NC1_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10342	22638	35831	1.01	4.0E-10	AI287342.1	EST_HUMAN	exp3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
948	13560	26074	1.85	3.0E-10	N38113.1	EST_HUMAN	y92708.s1 Soares melanocyte ZN1H1M Homo sapiens cDNA clone IMAGE:272863 3' similar to contains L1 H L1 repetitive element ;
1395	13989		4.43	3.0E-10	AY006150.1	NT	Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
4833	17218	28867	1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4833	17218	28868	1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5846	18274	30748	0.92	3.0E-10	N50109.1	EST_HUMAN	yz11g08.s1 Soares_multiple_sclerosis_ZN1H1MSP Homo sapiens cDNA clone IMAGE:282782 3'
6350	18855	31734	1.87	3.0E-10	P20350	SWISSPROT	RHOMBOID PROTEIN (VEINLET PROTEIN)
6492	19093	31877	2.86	3.0E-10	BE302870.1	EST_HUMAN	ba176d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
7737	20245	33136	2.3	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB1 Homo sapiens cDNA clone CBFBGD08 5'
7737	20245	33137	2.3	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB1 Homo sapiens cDNA clone CBFBGD08 5'
8695	21204	34122	1.08	3.0E-10	H87208.1	EST_HUMAN	y874b12.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER28 repetitive element ;
8979	21517	34442	1.81	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
8979	21517	34443	1.81	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9284	21790		0.86	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10359	22853		2.13	3.0E-10	T85991.1	EST_HUMAN	ye11e12.r1 Stratiogene lung (R837210) Homo sapiens cDNA clone IMAGE:80308 5'
10485	22879		1.71	3.0E-10	AA788294.1	EST_HUMAN	n28g03.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12415	24598	30911	3.44	3.0E-10	BE178517.1	EST_HUMAN	IL3-H10618-110500-139-E07 HT0618 Homo sapiens cDNA
38	12717	25178	92.79	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
38	12717	25177	92.79	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1942	14528		2.33	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
3015	15631		0.66	2.0E-10	BF875047.1	EST_HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5971	18582		7.24	2.0E-10	Q28840	SWISSPROT	(HPRG)
6398	18001	31779	1.42	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7414	18939	32803	7.79	2.0E-10	BE791082.1	EST_HUMAN	601588208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3840824 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7958	20468	33407	0.54	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7958	20468	33408	0.54	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8228	21742		0.85	2.0E-10	BF434585.1	EST_HUMAN	7078d08.x1 NCL_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:3842303 3' similar to contains L1.13 L1 repetitive element:
1556	14148		2.28	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-280300-001-401 SN0038 Homo sapiens cDNA
1650	14242	26776	2.41	1.0E-10	AW652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2618	15180		1.78	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191189-058-e09 CT0225 Homo sapiens cDNA
3548	16152	28634	0.73	1.0E-10	AW832812.1	EST_HUMAN	QV2-TT0003-161189-013-g10 TT0003 Homo sapiens cDNA
3593	16197		0.82	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3911	16197		0.80	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4087	16883		6.83	1.0E-10	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4207	16786	28243	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4207	16786	28244	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4214	16803	29253	1.95	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4249	16837		2.53	1.0E-10	MA30628.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, test exon
5343	17904		1	1.0E-10	AF797745.1	EST_HUMAN	w882704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.1 MER31 repetitive element:
8182	20723	33637	1.08	1.0E-10	AW408990.1	EST_HUMAN	FB_9A4 Fetal brain library Homo sapiens cDNA
8589	21128		1.03	1.0E-10	AL288340.1	EST_HUMAN	qtn04610.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element:
10103	22588		4.16	1.0E-10	AA081888.1	EST_HUMAN	zn23p06.r1 Striatogene neuroepithelium NT2RAM1 637234 Homo sapiens cDNA clone IMAGE:548314 5'
10793	23316	36325	3.47	1.0E-10	AL038280.1	EST_HUMAN	cy65f03.x1 Soares_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
11672	18038		1.58	1.0E-10	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
283	12839	25425	0.98	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2152	14729	27302	6.73	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
2152	14729	27303	6.73	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
3430	16038	28520	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	16038	28521	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4588	17182	29828	0.89	9.0E-11	AA775985.1	EST_HUMAN	ae7801.s1 Strategene echizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5763	18389		3.77	8.0E-11	BE079780.1	EST_HUMAN	RC8-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
10058	22553	35548	0.98	9.0E-11	AA324960.1	EST_HUMAN	EST17872 Cerebellum II Homo sapiens cDNA 5' end
10058	22553	35549	0.98	9.0E-11	AA324960.1	EST_HUMAN	EST17872 Cerebellum II Homo sapiens cDNA 5' end
12059	24342	30889	3.52	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506808 5'
3150	15764		0.38	8.0E-11	H10071.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4035	16833	20102	0.68	8.0E-11	AI478817.1	EST_HUMAN	hm54d08.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161838 3'
4117	16711	28165	5.2	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Wellmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255288 3'
1487	14088	26829	2.94	7.0E-11	AA330842.1	EST_HUMAN	EST134382 Embryo, 8 week I Homo sapiens cDNA 5' end
3838	16537	28004	0.84	7.0E-11	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8435	20875	33889	2.91	7.0E-11	AF163894.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22824		1.1	7.0E-11	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12208	24430		1.52	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBAC08 5'
437	13070	25568	5.57	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
437	13070	25567	5.57	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6822	19412	32228	1.03	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7880	20191	33080	3.29	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8305	20848	33769	3.25	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCA5C08 5'
12	12891	25147	0.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3411	12891	25147	1.29	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4312	16898	26343	1.04	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6838	18235	32037	3.02	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7537	20057	32831	12.3	5.0E-11	11418799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1446	14038		1.41	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2818	15368	27937	8.36	4.0E-11	BE885600.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908285 5'
2897	15613	28093	1.17	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4725	17306	29750	0.93	4.0E-11	D44666.1	EST_HUMAN	HUMSUP068 Human brain cDNA Homo sapiens cDNA clone 069
6802	19189	32005	3.5	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7409	18934		4.08	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9316	21830		1.44	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-008 HT0256 Homo sapiens cDNA
9580	22080	35045	0.91	4.0E-11	AI8009763.1	EST_HUMAN	H82g12.x1 NCI_CGAP_Bmt23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP-ZK353.1
12275	24478	30937	1.36	4.0E-11	11545732	NT	CE00385; Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1538	14130	28886	3.78	3.0E-11	6678077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4363	18950		1.47	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
985	13607	26121	1.64	2.0E-11	AI150502.1	EST_HUMAN	q30c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1227	13828	26342	5.04	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element;
1227	13828	26343	5.04	2.0E-11	R24807.1	EST_HUMAN	Y43a12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1655	14247	26780	6.04	2.0E-11	L17432.1	NT	Y43a12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1655	14247	26781	6.04	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and effector receptor-like protein
1659	14252	26786	1.09	2.0E-11	AI126371.1	EST_HUMAN	COR3beta (COR3beta) genes, complete cds
3230	15842	26323	6.98	2.0E-11	P10263	SWISSPROT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and effector receptor-like protein
3368	15878	26453	0.78	2.0E-11	AI478817.1	EST_HUMAN	COR3beta (COR3beta) genes, complete cds
3409	18018	28487	0.65	2.0E-11	Q10473	SWISSPROT	q51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:U02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11 L1 repetitive element;
3544	18148		1.01	2.0E-11	AF20503.1	NT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
4539	17123		0.89	2.0E-11	BE065537.1	EST_HUMAN	tm54c09.x1 NCI_CGAP_K411 Homo sapiens cDNA clone IMAGE:2161836 3'
4711	17203		0.65	2.0E-11	AL183227.2	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
5070	17843		1.37	2.0E-11	BE062558.1	EST_HUMAN	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAc:POLYPEPTIDE, N-
6284	18882	31661	1.2	2.0E-11	AW877808.1	EST_HUMAN	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAc-T1)
6452	18053	31838	2.02	2.0E-11	AA581028.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5
7246	19775	32632	0.78	2.0E-11	BF592845.1	EST_HUMAN	RC3-BT0316-170200-074-e05 BT0316 Homo sapiens cDNA
7823	20365		0.68	2.0E-11	P37072	SWISSPROT	Homo sapiens chromosome 21 segment HS21C027
							QV2-BT0256-261089-014-e01 BT0256 Homo sapiens cDNA
							QV2-P10073-280300-109-h08 P10073 Homo sapiens cDNA
							nc83k05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW-PR18_YEAST
							P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18;
							797c03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3442565 3'
							QLFACTORY RECEPTOR-LIKE PROTEIN COR6

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8150	21685		1.27	2.0E-11	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10184	22678	35671	4.8	2.0E-11	Q13608	SWISSPROT	OLFACTORY RECEPTOR 6T1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10409	22803	35889	0.79	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10409	22803	35900	0.79	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10982	23506	36538	2.41	2.0E-11	AA035388.1	EST_HUMAN	z427g02.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784.3
10982	23508	36539	2.41	2.0E-11	AA035388.1	EST_HUMAN	z427g02.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784.3
11805	25020		2.8	2.0E-11	AA704195.1	EST_HUMAN	z427g02.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784.3
11836	24200		2.48	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
11880	24218	31043	2.25	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070800-372-g01 TN0140 Homo sapiens cDNA
12135	24388		2.03	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12283	24482		5.24	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12628	24707		3.57	2.0E-11	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13325	25812	2.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
818	13434	25839	0.84	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1259	13856	26372	2.96	1.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1548	14138		1.88	1.0E-11	AF118974.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2171	14748	27317	2.61	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3548	16150	28630	0.83	1.0E-11	BE004315.1	EST_HUMAN	GM0-BN0105-170300-282-d12 BN0105 Homo sapiens cDNA
4005	17480		0.97	1.0E-11	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5535	18167	30581	15.03	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5987	18617	31353	0.8	1.0E-11	BF222846.1	EST_HUMAN	7p57d01.x1 NC1_CGAP_P128 Homo sapiens cDNA clone IMAGE:3848945.3 similar to contains MER10.b3
8143	20684	33598	3.16	1.0E-11	4885546	NT	MER10 repetitive element
8517	21056	33979	4.89	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHIF2) mRNA
8978	21518	34440	1.38	1.0E-11	BF365119.1	EST_HUMAN	Y73d08.1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28168.5
8978	21518	34441	1.38	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1148-250900-423-e03 NN1148 Homo sapiens cDNA
11187	23674	36721	2.46	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA
2878	15595	28075	0.67	9.0E-12	P20742	SWISSPROT	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977.5
9713	22211	35184	5.83	9.0E-12	AL163300.2	NT	PREGNANCY ZONE PROTEIN PRECURSOR
9713	22211	35185	5.83	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9261	21787		1	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
11911	24249		4.51	8.0E-12	AJ271736.1	NT	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
4766	17347	28796	1.88	7.0E-12	Q05904	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2 34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34)

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	23759	36815	12.18	7.0E-12	AA704735.1	EST_HUMAN	z223g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3601	16205		0.72	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4440	17026	29468	10.25	6.0E-12	AA732516.1	EST_HUMAN	nz88111.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
8928	21464	34380	0.92	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9395	21818		1.8	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER29.12
1081	13688	28188	2.85	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Strabagene (cat836208) Homo sapiens cDNA clone HFB0V33
3437	16045	28528	1.19	5.0E-12	BE047779.1	EST_HUMAN	tz42005.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291217 5'
3790	16390	28555	6.69	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6172	18784	31550	5.99	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6172	18784	31551	5.99	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6817	19214	32019	9.82	5.0E-12	AW974780.1	EST_HUMAN	EST388350 IMAGE resequences, MAGN Homo sapiens cDNA
7089	19448	32264	1.12	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7108	19448	32264	1.14	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8171	20712	33628	1.43	5.0E-12	AA033745.1	EST_HUMAN	z01612.s1 Soares_fetal_heart_NIH19W Homo sapiens cDNA clone IMAGE:376718 3' similar to contains L1.13 L1 repetitive element
8802	21141		0.7	5.0E-12	AW887037.1	EST_HUMAN	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
8925	21453		0.99	5.0E-12	AL078581.1	EST_HUMAN	DKFZp434J0428_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0428 5'
9037	21574	34504	2.42	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9344	21858	34808	1.04	5.0E-12	P34882	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10176	22871		4.17	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10286	22761	35748	0.87	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10461	22855	35968	2.12	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Doc), mRNA
265	12923	25408	3.53	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
268	12923	25409	4.43	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'
4727	17308	29752	0.82	4.0E-12	A068984.1	EST_HUMAN	b28f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR-Q13539 Q13539 MARINER TRANSPOSASE;
7615	20128		0.7	4.0E-12	BF445140.1	EST_HUMAN	rad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.b2
8185	20726		2.2	4.0E-12	AF109907.1	NT	MER7 repetitive element;
8621	21160	34075	1.2	4.0E-12	AB042815.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
							Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10961	23476	36501	4.25	4.0E-12	AJ228043.1	NT	Homo sapiens 958 kb contig between AM1.1 and CBR1 on chromosome 21q22, segment 3/3
12180	24416		1.61	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
644	13267	25744	2.73	3.0E-12	AW341683.1	EST_HUMAN	h13401.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR-O14617 O14517 SMRP.;
644	13267	25745	2.73	3.0E-12	AW341683.1	EST_HUMAN	h13401.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR-O14517 O14517 SMRP.;
5643	18272	30746	1.18	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8316	20857	33783	0.52	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
9035	21572	34501	0.56	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10535	23072	36085	3.26	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10535	23072	36086	3.26	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1693	14265	26820	1.05	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120400-065-e05 UM0071 Homo sapiens cDNA
3513	16118	28598	0.67	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 8.2 (Krtap8-2), mRNA
4192	16781	26229	0.9	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4192	16781	26230	0.9	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4512	17096		2.58	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031169-087-e03 BT0281 Homo sapiens cDNA
6603	19200		1.54	2.0E-12	AW971857.1	EST_HUMAN	EST383948 IMAGE resequences, MAGL Homo sapiens cDNA
7227	19758	32613	2.97	2.0E-12	T08180.1	EST_HUMAN	EST06060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end
7382	18908	32773	1.21	2.0E-12	BE173035.1	EST_HUMAN	MFR0-HT0659-200400-016-e08 HT0559 Homo sapiens cDNA
7656	20168	33055	2.38	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7894	20436		0.6	2.0E-12	AV683827.1	EST_HUMAN	AV683827 GKC Homo sapiens cDNA clone GKCFZB04 5'
9232	21054		2.18	2.0E-12	AF198884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
9898	22393		11.42	2.0E-12	BE165960.1	EST_HUMAN	MFR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10408	22902	35888	0.69	2.0E-12	A1334130.1	EST_HUMAN	qq0702.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR-Q13538
11820	24190		2.46	2.0E-12	AL163263.2	NT	Q13538 ORF2: FUNCTION UNKNOWN.;
128	12796	25282	2.78	1.0E-12	AW627674.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
2031	14613		1.53	1.0E-12	A1871726.1	EST_HUMAN	h180a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.1
3106	15721	28191	1.33	1.0E-12	AF000991.1	NT	MER18 repetitive element;
3106	15721	28192	1.33	1.0E-12	AF000991.1	NT	wm51f07.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439463 3' similar to contains L1.b3 L1
3943	16541	26007	38.65	1.0E-12	AU132248.1	EST_HUMAN	repetitive element;
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
							Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
							AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	16541	28008	38.85	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6121	18736		1.85	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6192	18802		1.95	1.0E-12	Q8Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIA0861
6653	19249	32051	0.7	1.0E-12	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7170	19702	32549	1.74	1.0E-12	AF196884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7204	19735	32587	9.7	1.0E-12	AI248533.1	EST_HUMAN	qh68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848014 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7204	19735	32588	9.7	1.0E-12	AI248533.1	EST_HUMAN	qh68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848014 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8426	20986	33880	0.54	1.0E-12	U68059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S0P13S3
8639	21178	34008	1.18	1.0E-12	AA782323.1	EST_HUMAN	ec28d05.s1 Stragene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
11723	24130	37154	4.65	1.0E-12	AW962164.1	EST_HUMAN	EST374237 IMAGE resequences, MAGG Homo sapiens cDNA
11941	24273		1.6	1.0E-12	AI738592.1	EST_HUMAN	w83N08.x1 NCI CGAP Cor16 Homo sapiens cDNA clone IMAGE:2392095 3'
12097	24990		2.72	1.0E-12	AL163289.2	NT	Homo sapiens chromosome 21 segment HS21C068
12424	24809		2.02	1.0E-12	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4019	16617	28092	0.91	9.0E-13	AB072600.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9519	22019		3.1	9.0E-13	N68893.1	EST_HUMAN	zaz26006.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3'
746	13366	25860	4.58	8.0E-13	U28185.1	NT	Homo sapiens priin protein (PrP) gene, complete cds
746	13368	25861	4.58	8.0E-13	U28185.1	NT	Homo sapiens priin protein (PrP) gene, complete cds
1878	14464	27021	3.95	8.0E-13	U90017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8056	20508	33505	0.68	8.0E-13	AI894398.1	EST_HUMAN	wm31H09.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8056	20508	33506	0.68	8.0E-13	AI894398.1	EST_HUMAN	wm31H09.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
10051	22546		2.58	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11609	24052	37117	2.51	8.0E-13	U68080.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S6A3N2T, TCRBV13S8A2T, TCRBV6S8P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S8A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P
8178	20717		0.63	7.0E-13	Q85155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12212	24435		37.61	7.0E-13	BE78223.1	EST_HUMAN	001403285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
12448	24563		1.71	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
2149	14728	27290	6.02	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3384	15872		0.78	5.0E-13	R78338.1	EST_HUMAN	y6204.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:145759 5'
3444	16052		1.84	5.0E-13	AA435773.1	EST_HUMAN	z177a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Abu repetitive element:contains element MER22 repetitive element;
6958	19535	32358	0.68	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
10739	23264	36279	2.49	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1808	14493		3.69	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221089-001-e11 HT0224 Homo sapiens cDNA
2500	15084		1.71	4.0E-13	AF003529.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
4858	17438		1.03	4.0E-13	AA454054.1	EST_HUMAN	z149d07.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785489 5'
5774	18368	31113	5.09	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7257	19785	32841	1.07	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7807	20120	32897	0.81	4.0E-13	AA431529.1	EST_HUMAN	z178g12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA;
7705	20214		1.84	4.0E-13	N44281.1	EST_HUMAN	y633g05.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32895 A32895 t complex sterility protein - mouse;
8775	21314	34238	0.94	4.0E-13	AL043810.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434A0128 5'
9833	22429	35403	4.28	4.0E-13	AL289831.1	EST_HUMAN	q132d05.x1 NC1_CGAP_K165 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Abu repetitive element;
11048	23559	36585	1.91	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11048	23559	36586	1.91	4.0E-13	AA435819.1	EST_HUMAN	z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
192	12852		4.5	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
898	13512		4.67	3.0E-13	AA430310.1	EST_HUMAN	z168g08.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2408	14978	27550	1.08	3.0E-13	AL1271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2519	15083		6.72	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2687	15245	27812	2.75	3.0E-13	BF372682.1	EST_HUMAN	CM3-FT10100-140700-242-408 FT10100 Homo sapiens cDNA
3221	15633		3.1	3.0E-13	AA745844.1	EST_HUMAN	cb18d02.x1 NCI_OGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3551	16155	28637	1.04	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3551	16155	28638	1.04	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5730	18356	31060	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
5730	18356	31061	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
6143	18757	31515	0.88	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI_OGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN.;
7824	20366	33274	9.98	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8021	20563	33464	0.66	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re-reactive factor
8021	20563	33465	0.66	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re-reactive factor
10558	23092		4.07	3.0E-13	AJ084768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10924	23443	36464	2.91	3.0E-13	BE063506.1	EST_HUMAN	CM0-BT0281-031169-087-a03 BT0281 Homo sapiens cDNA
11469	23919	36868	2.49	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
161	12824	25312	2.56	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
260	12919	25406	2.22	2.0E-13	U23839.1	NT	Dario ratio fibroblast growth factor receptor 4 mRNA, complete cds
1313	13907	26427	8.94	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3038	15654	26133	0.96	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3038	15654	26134	0.96	2.0E-13	8824119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3320	15830	28407	1.2	2.0E-13	BF431898.1	EST_HUMAN	neb76005.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3555	16156	28842	1.14	2.0E-13	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4186	16776		1.9	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6271	18879	31647	5.27	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6805	18639	32475	7.42	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
10355	22649	35943	4.58	2.0E-13	5031868	NT	Homo sapiens mab-21 (C. elegans) like 1 (MAB21L1) mRNA
11683	24236		20.31	2.0E-13	AW802155.1	EST_HUMAN	CMO-NIN0001-100300-274-011 NN0001 Homo sapiens cDNA
313	12967	25455	1.8	1.0E-13	S74128.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
921	13534	26052	4.35	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1381	13974	26502	1.01	1.0E-13	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2068	14648	27220	1.8	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3
4116	16710		2.21	1.0E-13	AA324394.1	EST_HUMAN	THR repetitive element;
4698	17278	28724	1.51	1.0E-13	BF340887.1	EST_HUMAN	EST127235 Carabellum II Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7851	20383	33296	0.77	1.0E-13	AA577812.1	EST_HUMAN	602038008F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185986 5'
7851	20383	33297	0.77	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
10002	22497		0.9	1.0E-13	O15481	SWISSPROT	repetitive element; contains element MER24 repetitive element;
10202	22697	35691	0.52	1.0E-13	AF300701.1	NT	repetitive element; contains element MER24 repetitive element;
11266	23786	36842	15.07	1.0E-13	BF108755.1	EST_HUMAN	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
11714	24124		1.87	1.0E-13	AV715377.1	EST_HUMAN	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
12393	24553		4.28	1.0E-13	AJ271735.1	NT	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element;
355	13004	25488	4.61	9.0E-14	AA781159.1	EST_HUMAN	AV715377 DC8 Homo sapiens cDNA clone DCBAIE03 5'
359	13005	25489	2.07	9.0E-14	AA781159.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
2545	15109		3.84	9.0E-14	AW861577.1	EST_HUMAN	qj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
2627	15189	27757	1.41	9.0E-14	AJ133127.1	NT	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2627	15189	27758	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2782	15335	27905	3.29	9.0E-14	AB038162.1	NT	Homo sapiens TRF gene cluster for trefoil factor, complete cds
3145	15759	28225	4.32	9.0E-14	AW513286.1	EST_HUMAN	hcs4h05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3'
3275	13004	25488	0.71	9.0E-14	AA781159.1	EST_HUMAN	qj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
3886	16484	28928	7.24	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4870	17448	29697	1.77	9.0E-14	AJ002153.1	NT	Sagittarius oedipus gene for seminal vesicle secreted protein semenogelin I

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3545	16149		0.97	8.0E-14	BE468263.1	EST_HUMAN	h271c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4028	16627		3.29	8.0E-14	R70269.1	EST_HUMAN	Y72x03.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:144786 3'
9369	20308	33211	36.57	8.0E-14	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9479	21878	34826	4.61	8.0E-14	AA218316.1	EST_HUMAN	zq17c10.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628870 3'
11310	23803		4.45	8.0E-14	BE062556.1	EST_HUMAN	QV2-BT0258-261089-014-e01 BT0258 Homo sapiens cDNA
12106	24368	30972	2.07	8.0E-14	AI688118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326143 3'
							x467a10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823146 3' similar to contains MER10.12
1671	15447		2.78	7.0E-14	AW151973.1	EST_HUMAN	MER10 repetitive element;
8851	21390		0.54	7.0E-14	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C085
390	13038	25626	14.21	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9736	22234	35212	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9736	22234	35213	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
646	13269	25747	5.26	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
							x403b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
5209	17774	30197	1.53	5.0E-14	AW073781.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5724	18350	31053	4.91	5.0E-14	P08547	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1162	15434		1.61	4.0E-14	P04828	SWISSPROT	Homo sapiens LGMD2B gene
1820	14505	27062	3.86	4.0E-14	AJ007873.1	NT	2k67a06.r1 Soares_pregnant_luteus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
3816	16416		0.84	4.0E-14	AA048502.1	EST_HUMAN	Yy73c12.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:278180 3' similar to contains L1.13 L1 repetitive element;
4379	16966	28412	0.9	4.0E-14	N46328.1	EST_HUMAN	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
7899	20441		0.49	4.0E-14	X87344.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11633	24073	37135	1.91	4.0E-14	P08548	SWISSPROT	wm08c03.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
12457	25107		4.37	4.0E-14	AI886224.1	EST_HUMAN	R.norvegicus mRNA for GPC2 protein
985	13597	28110	1.28	3.0E-14	X85466.1	NT	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
5059	17632	30075	0.74	3.0E-14	AW285354.1	EST_HUMAN	

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6832	19422	32237	1.08	3.0E-14	AI420786.1	EST_HUMAN	ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE.;
6832	19422	32238	1.08	3.0E-14	AI420786.1	EST_HUMAN	ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE.;
8722	21281	34181	0.96	3.0E-14	N42165.1	EST_HUMAN	y07b10.1 Scores melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:270523 5'
10872	23383	38408	2.75	3.0E-14	BE88016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11118	17832	30076	9.84	3.0E-14	AW285354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_H1111 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
12689	24884		1.84	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
413	13048	25539	2.51	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
413	13048	25540	2.51	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
719	15422	25828	9.8	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2431	14898		1.48	2.0E-14	AW372888.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
2504	15068		1.07	2.0E-14	7657528	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
2567	15131	27689	1.03	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
2689	15256		0.88	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5715	18341	30847	0.95	2.0E-14	BF380861.1	EST_HUMAN	IL2-JT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5804	18428	31148	0.8	2.0E-14	AI312351.1	EST_HUMAN	ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5895	18517	31242	2.86	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6863	18540		0.88	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7329	18856	32719	1.12	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-Q4
7518	20038	32808	20.34	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7518	20038	32807	20.34	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
9831	22329	35311	0.54	2.0E-14	AI878795.1	EST_HUMAN	wf58g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2482034 3' similar to contains Alu repetitive element
10659	23191	36206	4.65	2.0E-14	AW139800.1	EST_HUMAN	U1-H-BH1-adv-a-10-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12668	24968		3.3	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
12817	15068		1.99	2.0E-14	7657528	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
1105	13708	28218	1.89	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1452	14044	28572	6.88	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1452	14044	28573	6.88	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2044	14628	27195	7.63	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from fibrin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's

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2228	14803	27374	5.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2453	15020	27591	5.89	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2971	15597	28069	1.51	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHIRP-II)
3203	15816	28280	3.91	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3203	15815	28291	3.91	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3955	16553	29022	2.1	1.0E-14	AA882984.1	EST_HUMAN	ae88c12.s1 Striatogene schizob brain S11 Homo sapiens cDNA IMAGE:371350 3'
4572	17155	29599	1.71	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5977	18597	31332	2.03	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6778	24770	32183	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6778	24770	32184	12	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1620	14213	28744	1.19	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2217	14782		1.39	9.0E-15	AF196778.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel α)
7507	20029	32892	3.77	9.0E-15	P21416	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7969	20501	33410	1.38	9.0E-15	BE603559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980158 5'
12580	24680		1.78	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2837	13138		1.17	8.0E-15	BE261482.1	EST_HUMAN	601148832F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7233	19783	32819	1.29	7.0E-15	BF035327.1	EST_HUMAN	60145831F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882088 5'
10331	22825		2.53	7.0E-15	AW241958.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element:
11776	24184		1.78	7.0E-15	AA284485.1	EST_HUMAN	zs57d08.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb.L21834 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1.1 L1 repetitive element;
1031	13641	26156	6.29	6.0E-15	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6077	18694	31440	1.18	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6077	18694	31441	1.18	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
11182	25128		1.86	6.0E-15	AW636843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
12648	24722		1.3	6.0E-15	BF432200.1	EST_HUMAN	ne881c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
435	13068	25563	5.19	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2789	15342	27912	2.35	6.0E-15	U61328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3515	16120		1.09	5.0E-15	AW286817.1	EST_HUMAN	UIH-BW0-qib-g-10-Q-UJ.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731219 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5289	17881		1.28	5.0E-15	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10555	23091		2.72	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
452	12881	25137	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6771	18384	32173	0.79	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
10940	20287	33184	2.54	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10940	20287	33185	2.54	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4287	16883		7.28	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5060	17833		0.57	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
5178	17748	30175	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5179	17748	30176	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6804	18638		1.41	3.0E-15	Q84825	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7323	18650	32711	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7323	18650	32712	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9839	22337		2.32	3.0E-15	AA807128.1	EST_HUMAN	cc38a07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element ;
10673	23205	36218	3.36	3.0E-15	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12114	24987		1.36	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
271	12928	25415	4.1	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
391	13037	25528	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
391	13037	25527	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2410	14978	27552	1.44	2.0E-15	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER28.b3 MER28 repetitive element ;
2410	14978	27553	1.44	2.0E-15	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER28.b3 MER28 repetitive element ;
3559	16163	28845	0.73	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3559	16163	28846	0.73	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4142	16734	28188	0.95	2.0E-15	AW238468.1	EST_HUMAN	xp28801.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1 repetitive element ;
4729	17310		2.72	2.0E-15	A1806335.1	EST_HUMAN	wf07708.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2349823 3' similar to TR:Q61043
5332	17883	30306	0.93	2.0E-15	P13983	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
5332	17893	30307	0.93	2.0E-15	P13983	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
6329	18935	31711	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5'
6329	18935	31712	1.02	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5'
7168	19700		1.37	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7315	18842	32703	2.51	2.0E-15	AA704195.1	EST_HUMAN	z177e03.a1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460824 3'
7427	19851	32816	4.48	2.0E-15	W05084.1	EST_HUMAN	z177d10.11 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:288875 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;
8837	21376	34300	2.62	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9002	21539	34468	0.87	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9002	21539	34469	0.87	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9325	21839	34790	1.13	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201088-078-a12 HT0244 Homo sapiens cDNA
9325	21839	34791	1.13	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201088-078-a12 HT0244 Homo sapiens cDNA
10718	23246		3.59	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12487	16163	28845	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12487	16163	28846	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2803	15355		2.08	1.0E-15	A1888984.1	EST_HUMAN	b28h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
3048	15882	28143	1.24	1.0E-15	BE043594.1	EST_HUMAN	hk40e02.y1 NCI_CGAP_Ox64 Homo sapiens cDNA clone IMAGE:2888182 5'
3178	16789	28261	1.06	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6510	19110	31868	1.71	1.0E-15	T95763.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
7080	19652		1.91	1.0E-15	BE074217.1	EST_HUMAN	GV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
7105	19445	32262	0.77	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8174	20715	33631	0.88	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8359	20899	33819	4.97	1.0E-15	A1200978.1	EST_HUMAN	qf68h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8359	20899	33820	4.97	1.0E-15	A1200978.1	EST_HUMAN	qf68h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8969	21507	34428	0.51	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8972	21510	34432	1.99	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9171	21748	34681	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9550	22050	35012	1.18	1.0E-15	AA884653.1	EST_HUMAN	chr37c03.s1 NCI_CGAP_K148 Homo sapiens cDNA clone IMAGE:1469872 3' similar to contains L1.13 L1 repetitive element;
10698	23228	38242	6.66	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
12664	24820	30782	9.35	1.0E-15	A1783944.1	EST_HUMAN	t31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element
4417	17002		0.63	9.0E-16	BF689487.1	EST_HUMAN	802120192F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277422 5'
4802	17185	29632	1.11	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
10873	23394	38409	2.68	9.0E-16	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23F05
5880	18502	31228	0.73	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7379	19905	32769	1.36	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE M) (PAD-R4)
7379	19905	32770	1.36	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE M) (PAD-R4)
12509	24916		33.75	7.0E-16	T04149.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
2186	14762		29.26	6.0E-16	AW872611.1	EST_HUMAN	ye28c12.11 Stratiogene lung (8037210) Homo sapiens cDNA clone IMAGE:118062 5'
5436	17891	30397	0.94	6.0E-16	BF365702.1	EST_HUMAN	EST384702 MAGE resequences, MAGL Homo sapiens cDNA
1539	14131	26687	1.21	5.0E-16	AJ251154.1	NT	QV2-NT0048-160800-316-412 NT0048 Homo sapiens cDNA
2705	15262	27829	2.6	5.0E-16	AA982176.1	EST_HUMAN	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
11398	23848	36914	3.76	5.0E-16	BF217988.1	EST_HUMAN	cd80c04.a1 Soares_t041_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
12806	24680		4.86	5.0E-16	11418127	NT	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104128 5'
2281	14855		1.23	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2419	14987	27561	1.68	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEI1 and PWP2, complete and partial cds
2419	14987	27562	1.68	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
3503	18108	26584	6.73	4.0E-16	Q16653	SWISSPROT	QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA
4223	18811	29258	4.28	4.0E-16	BE083675.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4223	18811	29259	4.28	4.0E-16	BE083675.1	EST_HUMAN	PMA4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
7698	20207	33094	37.48	4.0E-16	AL163284.2	NT	PMA4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
9219	21736	34678	1.44	4.0E-16	11423191	NT	Homo sapiens chromosome 21 segment HS21C084
11088	23808	36948	1.68	4.0E-16	AV730030.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
							AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11800	24180		1.34	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11887	24232		13.76	4.0E-16	C05847.1	EST_HUMAN	C05847 Human pancreatic islet Homo sapiens cDNA clone hbc3355
11887	24239	31008	2.91	4.0E-16		NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12178	24414		1.8	4.0E-16	R18591.1	EST_HUMAN	Y68b11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5'
138	12803	25292	0.93	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
138	12803	25293	0.93	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
491	13124		1.24	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
501	13133		2.35	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1501	14093	26632	1.81	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
3004	16820	28097	4.2	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4007	16905	29079	0.81	3.0E-16	T08169.1	EST_HUMAN	EST00600 Infant Brain, Benito Soares Homo sapiens cDNA clone HIBBA13 5' and
4031	16828		1.07	3.0E-16	U03887.1	NT	Human BXP-20 gene
4689	17271	29720	0.97	3.0E-16	AW160828.1	EST_HUMAN	eu76606.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to SW:KID1_MOUSE Q81751 RENAL TRANSCRIPTION FACTOR KID-1;
5077	17650	30091	1.14	3.0E-16	AV681393.1	EST_HUMAN	AV681393 GLC Homo sapiens cDNA clone GLCGSA01 3'
6482	18116		0.9	3.0E-16	AA077226.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5801	18428	31144	1.57	3.0E-16	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8592	21131	34047	4.08	3.0E-16	A1002838.1	EST_HUMAN	en08h05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR_b2 THR repetitive element;
9805	22303		0.84	3.0E-16	BF880617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10027	22522	35518	5.15	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12837	25078	30516	9.33	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
1007	13818		1.38	2.0E-16	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
2429	14996		1.01	2.0E-16	AA621791.1	EST_HUMAN	af06d04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2713	15270		1.53	2.0E-16	J03081.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4257	16843	29292	1.34	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
5370	17930	30344	0.57	2.0E-16	BE001178.1	EST_HUMAN	RC3-BT0048-131188-003-H12 BT0048 Homo sapiens cDNA
6839	19429	32245	0.89	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7701	20210	33097	0.76	2.0E-16	A470723.1	EST_HUMAN	U18e11.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
7908	20450	33357	1.81	2.0E-16	A1732837.1	EST_HUMAN	nc4706.x6 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 ;contains MER7.t1 MER7 repetitive element.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8099	20840	33551	0.7	2.0E-18	BE89028.1	EST_HUMAN	782H09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3'
8099	20840	33552	0.7	2.0E-18	BE89028.1	EST_HUMAN	782H09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3'
8464	21004	33921	0.6	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-508-601 PT0034 Homo sapiens cDNA
8464	21004	33922	0.6	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-508-601 PT0034 Homo sapiens cDNA
10808	23331	36343	2.71	2.0E-18	5802145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
197	12857	25339	2.56	1.0E-18	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
405	13080		29.83	1.0E-18	AA628692.1	EST_HUMAN	af39g11.s1 Soares_t048_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
2014	14598	27159	1.78	1.0E-18	BF327942.1	EST_HUMAN	QV0-BND148-070700-283-a10 BN0148 Homo sapiens cDNA
5896	18518	31243	0.85	1.0E-18	AF163984.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	19163		27.68	1.0E-18	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6888	19284	32087	2.77	1.0E-18	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7558	19163		6.98	1.0E-18	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9207	21724	34867	1.15	1.0E-18	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
3802	18402	28868	2.48	9.0E-17	AW900048.1	EST_HUMAN	GM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
6824	18414		1.94	9.0E-17	AI392884.1	EST_HUMAN	tg22a-11.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2108524 3' similar to contains MER28.12 MER28 repetitive element;
8052	20584		4.65	9.0E-17	AW150257.1	EST_HUMAN	xq48g12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630850 3' similar to contains OFR.12 OFR repetitive element;
10124	22819		2.1	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1058	13681		1.56	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-a01 OT0032 Homo sapiens cDNA
3961	16559		0.7	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5771	24748	31111	3.55	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-080300-003-a04 HT0559 Homo sapiens cDNA
7319	18846		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1505	14097		3.4	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5528	18158		2.97	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6789	16380	32186	7.15	7.0E-17	AF22843.1	NT	Mus musculus WNT-2 gene, partial cds; putative enkyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
217	12878	25365	7.43	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-a04 HN0003 Homo sapiens cDNA
6455	18056	31841	1.68	8.0E-17	AW862772.1	EST_HUMAN	h181d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878695 3' similar to contains L1.12 L1 repetitive element;
10182	22887	35880	0.52	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
446	12675	25131	2.78	5.0E-17	T64110.1	EST_HUMAN	y05h08.r1 Stratiogene lung (4937210) Homo sapiens cDNA clone IMAGE:79839 5'
7580	20101	32870	1.82	5.0E-17	T61043.1	EST_HUMAN	y126h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
9284	21884	34829	1.12	4.0E-17	AW128165.1	EST_HUMAN	yf20e04.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11365	23817	36878	2.17	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11816	24188		2.36	4.0E-17	A1073548.1	EST_HUMAN	04f5e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
1540	14132		1.03	3.0E-17	D14547.1	NT	Q16530 PMSS3 MRNA ; contains MER10.12 MER10 repetitive element ;
2146	14723	27295	1.28	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3227	15839		1.41	3.0E-17	P35410	EST_HUMAN	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3704	16305	28773	1.24	3.0E-17	BE326522.1	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3704	16305	28774	1.24	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181889 3'
5181	17747		1.02	3.0E-17	BF511268.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181889 3'
8212	20753	33687	1.09	3.0E-17	N68451.1	EST_HUMAN	UI-H-B14-adj-c-08-0-J1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
9618	22118	35081	4.54	3.0E-17	AB026898.1	NT	z14802.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282491 3' similar to contains PTR5.13 PTR5 repetitive element ;
10282	22777	35767	0.65	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10282	22777	35768	0.65	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
11775	24163		3.77	3.0E-17	11417888	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
375	13024	25510	3.38	2.0E-17	A1270080.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
378	13024	25510	2.68	2.0E-17	A1270080.1	EST_HUMAN	q63a08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element;
1025	13036		1.12	2.0E-17	AA722832.1	EST_HUMAN	q63a08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element;
2490	15055	27627	2.43	2.0E-17	Q28983	SWISSPROT	z61d04.s1 Soares_fetal_heart_NBH10W Homo sapiens cDNA clone IMAGE:399751 3'
2490	15055	27628	2.43	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2956	15572	28049	8.06	2.0E-17	P12036	SWISSPROT	ZONADHESIN PRECURSOR
5568	18200	30648	1.57	2.0E-17	M27885.1	NT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5569	18200	30649	1.57	2.0E-17	M27885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6410	18013		1.8	2.0E-17	AF055068.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6816	19213		1.68	2.0E-17	AL134881.1	EST_HUMAN	Homo sapiens MHC class I region
7773	20282	33178	0.65	2.0E-17	AB037839.1	NT	DKFZp762J0610 .r1 762 (synonym: hmls2) Homo sapiens cDNA clone DKFZp762J0610 5'
							Homo sapiens mRNA for KIAA1418 protein, partial cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8028	20570	33474	1.64	2.0E-17	Q85156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OL3
8394	20834	33856	1.15	2.0E-17	AA300840.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' and similar to glycogenin
9783	22281	35287	2.45	2.0E-17	BE208888.1	EST_HUMAN	600944680F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860815 5'
9818	22318	35297	3.36	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9818	22316	35298	3.36	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10180	22855	35650	7.23	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10281	22776	35765	0.58	2.0E-17	P88063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10281	22776	35768	0.58	2.0E-17	P88063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10306	22800	35791	0.63	2.0E-17	AI798802.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10306	22800	35782	0.63	2.0E-17	AI798802.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
780	13399	25902	3.38	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1746	14338		1.2	1.0E-17	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1804	14394	26839	2.89	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2182	14739	27309	2.11	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2373	14943	27616	1.86	1.0E-17	U78410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3625	16228		0.89	1.0E-17	AF224668.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4217	16805		8.46	1.0E-17	R09942.1	EST_HUMAN	Y30a07.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
6759	19352	32161	1.55	1.0E-17	AI185842.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6759	19352	32162	1.55	1.0E-17	AI185842.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7146	19678	32520	1.28	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8528	21067	33986	1.23	1.0E-17	BE082744.1	EST_HUMAN	QV0-BT0263-101299-072-d07 BT0263 Homo sapiens cDNA
8919	22415	35390	0.94	1.0E-17	AW986338.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11295	23747	36805	1.82	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2510	15074	27647	1.13	9.0E-18	AA174078.1	EST_HUMAN	zp18g12.s1 Striatogene fetal retina 93/202 Homo sapiens cDNA clone IMAGE:60862 3'
9418	21927		3.03	9.0E-18	AI472167.1	EST_HUMAN	ig6c403.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3854	16452	28915	1.56	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
371	13020	25504	32.68	7.0E-18	AW316978.1	EST_HUMAN	xc10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20868 60S
371	13020	25505	32.68	7.0E-18	AW316978.1	EST_HUMAN	xc10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20868 60S
7469	19891	32854	0.96	7.0E-18	AW887542.1	EST_HUMAN	RC3-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12308	13020	25504	5.28	7.0E-18	AW316978.1	EST_HUMAN	xc10604.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
12308	13020	25506	5.28	7.0E-18	AW316978.1	EST_HUMAN	xc10604.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3334	15844	28419	1.38	6.0E-18	X71791.2	NT	Rattus norvegicus partial GdhFr-1 gene for glia-derived neuroprotease within 1. enhancer region
4857	17435		3.95	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8182	20733		2.75	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83448), mRNA
8289	20830	33751	0.6	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11014	23528	36564	1.87	6.0E-18	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11209	23713	36767	1.9	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
11591	24034		2.22	6.0E-18	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83091), mRNA
12041	24328	30895	2.24	6.0E-18	U87828.1	NT	Human acornitide hydratase (ACO2) gene, exon 4
1187	13788	26299	11.3	5.0E-18	AI280214.1	EST_HUMAN	qm65g11.x1 Soares placenta 8t6weeks_2NHP8t69W Homo sapiens cDNA clone IMAGE:1893688 3' similar to contains Alu repetitive element;
5284	17848	30273	0.94	5.0E-18	D61517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-411F05 5'
5477	18111	30520	1.03	5.0E-18	AF087813.1	NT	Human endogenous retrovirus HERV-P-T47D
8854	21193	34111	4.82	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0181-221089-002-c08 HT0181 Homo sapiens cDNA
10857	23378	36396	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
10857	23378	36397	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12170	24409		6.6	6.0E-18	AW887182.1	EST_HUMAN	MRI-SN0035-060-400-001-g11 SN0035 Homo sapiens cDNA
12531	24844		51.19	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLOCGA02 3'
130	12797	25283	1.98	4.0E-18	BE044076.1	EST_HUMAN	hc38r04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
130	12797	25284	1.98	4.0E-18	BE044076.1	EST_HUMAN	hc38r04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1754	14344	28890	8.14	4.0E-18	AA621814.1	EST_HUMAN	nc24f11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M28328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1833	14517		0.92	4.0E-18	AI738592.1	EST_HUMAN	wf39r08.x1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:2392095 3'
2242	14817	27390	1.23	4.0E-18	Q06430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (BRANCHING ENZYME) (IGNT)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14817	27391	1.23	4.0E-18	Q06430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (H-BRANCHING ENZYME) (IGNT)
5568	18197	30843	2.32	4.0E-18	A017565.1	EST_HUMAN	cu23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3'
5568	18197	30844	2.32	4.0E-18	A017565.1	EST_HUMAN	cu23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3'
7787	20330		0.81	4.0E-18	AA746811.1	EST_HUMAN	nc04e08.s1 NCI_CGAP_AH1 Homo sapiens cDNA clone IMAGE:1268698 similar to contains L1.12 L1 repetitive element;
10884	23405	36424	7.68	4.0E-18	AA371807.1	EST_HUMAN	EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
882	13496	26015	18.02	3.0E-18	AA814106.1	EST_HUMAN	cb23h11.s1 NCI_CGAP_K145 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW_RS5_HUMAN
865	13576	26091	2.25	3.0E-18	BE088634.1	EST_HUMAN	PA6782 40S RIBOSOMAL PROTEIN S5.;
4022	16620	28093	1.25	3.0E-18	AL163247.2	NT	CMO-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
6917	19578	32405	6.98	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
12312	24504		8.85	3.0E-18	AW022015.1	EST_HUMAN	PMO-BN0081-100300-001-008 BN0081 Homo sapiens cDNA
272	12928	25410	2.57	2.0E-18	AW636820.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
1192	13793		197.1	2.0E-18	BE256097.1	EST_HUMAN	QV1-LT0038-150200-070-e07 LT0038 Homo sapiens cDNA
3157	15771	26238	1.15	2.0E-18	Q39575	SWISSPROT	601114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
5606	18235		3.99	2.0E-18	AA868610.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5687	18323	30823	3.16	2.0E-18	D14547.1	NT	ak53e07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5687	18323	30824	3.16	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.;
6038	18957		1.98	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6313	18920	31686	1	2.0E-18	X60456.1	NT	Human DNA, SINE repetitive element
6313	18920	31686	1	2.0E-18	X60456.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
6424	19027	31810	0.84	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for Interferon alpha/beta receptor
6460	19061	31847	7.53	2.0E-18	AW695853.1	EST_HUMAN	IL3-HT0819-220700-222-G12 HT0819 Homo sapiens cDNA
9960	22455	35437	1.39	2.0E-18	AW151673.1	EST_HUMAN	h04g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879884 3' similar to contains MER19.12 MER19 repetitive element;
9960	22455	35438	1.39	2.0E-18	AW151673.1	EST_HUMAN	h04g01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
10854	23375	36394	4.96	2.0E-18	AW470791.1	EST_HUMAN	MER10 repetitive element;
							x07e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
							MER10 repetitive element;
							h03g08.x1 NCI_CGAP_K12 Homo sapiens cDNA clone IMAGE:2875469 3' similar to contains THR.b3
							THR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11578	24026	37063	5.24	2.0E-18	AW151289.1	EST_HUMAN	xp7c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2830728 3' similar to contains MER8.b2
11970	13783		20.18	2.0E-18	BE256097.1	EST_HUMAN	MER8 repetitive element ; 601114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
4507	17091		0.85	1.0E-18	T85408.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
5558	18190	30806	1.91	1.0E-18	AV683405.1	EST_HUMAN	AV683405 GLC Homo sapiens cDNA clone GLDKE11 3'
5759	18385	31068	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5759	18385	31100	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6582	19180	31980	1.37	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8380	20820	33840	1.22	1.0E-18	AI148288.1	EST_HUMAN	cd69d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680503 3' similar to contains L1.11 L1 repetitive element ;
9813	22311	35283	4.45	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11918	24255	31011	4.39	1.0E-18	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
571	13202	25684	3.33	9.0E-19	AA281981.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
572	13202	25684	2.86	9.0E-19	AA281981.1	EST_HUMAN	MER19 repetitive element ;
7790	20333		5.83	9.0E-19	F09688.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
8822	21181	34078	2.46	9.0E-19	AL163203.2	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23F05
8822	21181	34077	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11007	23521	36556	3.02	9.0E-19	AB032069.1	NT	Homo sapiens chromosome 21 segment HS21C003
11678	13202	25684	28.32	9.0E-19	AA281981.1	EST_HUMAN	Homo sapiens mRNA for KIAA1143 protein, partial cds
1088	13891		1.38	8.0E-19	AW974002.1	EST_HUMAN	z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
8090	20631	33544	1	8.0E-19	BE158936.1	EST_HUMAN	MER19 repetitive element ;
2287	14861	27436	1.72	7.0E-19	4758139	NT	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
6584	19182	31982	1.91	7.0E-19	AF092090.1	NT	MR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA
7341	19868	32732	0.95	7.0E-19	P28444	SWISSPROT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
9025	22421	35395	0.47	7.0E-19	AB344681.1	EST_HUMAN	Rattus norvegicus cp151 mRNA, partial cds
11823	25088		2.85	7.0E-19	AA705684.1	EST_HUMAN	BETA CRYSTALLIN A2
3847	16446		1.21	6.0E-19	AW852930.1	EST_HUMAN	601c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
							360b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
							PMO-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4562	17145	28562	1.39	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4562	17145	28563	1.39	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4919	17494		1.15	6.0E-19	AJ271735.1	NT	Homo sapiens Xq psautofluorescent region; segment 1/2
6019	18638	31378	5.29	5.0E-19	Q00183	SWISSPROT	ZP-X) (RC55)
6365	18689	31747	0.79	5.0E-19	AW663302.1	EST_HUMAN	h77606.y1 NCI_QGAP_GU1 Homo sapiens cDNA clone IMAGE:2868767 5'
10322	22818	35812	0.66	5.0E-19	AJ297689.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11412	23863	36924	7.61	5.0E-19	AW163725.1	EST_HUMAN	x87602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2864171 3' similar to contains element MSRT1 repetitive element;
12544	24823		1.36	5.0E-19	U68060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S8A3N2T, TCRBV13S6A2T, TCRBV6S8P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12
580	13210	25688	0.85	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2707	15264	27831	1.25	4.0E-19	BF687362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
5583	18223	30872	1.1	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3919	16517	28982	1.58	3.0E-19	Q28897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3919	16517	28983	1.58	3.0E-19	Q28897	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4373	16660	29405	0.9	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4373	16660	29406	0.9	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4544	17128	28571	1.33	3.0E-19	AV708138.1	EST_HUMAN	AV708138 ADC Homo sapiens cDNA clone ADCAMA11 5'
6484	18118		0.8	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7418	18942		1.83	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9380	20319	33220	1.2	3.0E-19	X89685.1	NT	Mytilus mRNA for TPCP33 protein
12084	24347		16.44	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
2585	15157	27725	7.09	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4542	17128		1.28	2.0E-19	AI311783.1	EST_HUMAN	q961402.x1 NCI_QGAP_K45 Homo sapiens cDNA clone IMAGE:1915888 3' similar to TR-Q68398 Q68398 POL/ENV GENE:
8272	20813	33735	8.35	2.0E-19	AA012854.1	EST_HUMAN	z634c09.1 Soares retina N264HR Homo sapiens cDNA clone IMAGE:360880 5'
9823	22321	35308	0.81	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
507	13140		1.65	1.0E-19	BE408611.1	EST_HUMAN	801304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'